

T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.
A:Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A:Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*.
A:Reference number: A69580; MUID:98044033; PMID:9384377
A:Accession: F69735
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-213 <KUN>
A:Cross-references: UNIPARC:UPI00000336C9; GB:Z99114; GB:AL009126; NID:g2634230; PIDN:CA
A:Experimental source: strain 168
C:Genetics:
A:Gene: xynA
A:Map position: 175 degrees
C:Function:
A:Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xylans
A:Pathway: xylan degradation
C:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
C:Keywords: extracellular protein; glycosidase; hydrolase; polysaccharide degradation
F:1-28/Domain: signal sequence #status predicted <SIG>
F:29-213/Product: endo-1,4-beta-xylanase A #status experimental <MAT>
F:31-213/Domain: endo-1,4-beta-xylanase homology <XYL>
F:106/Active site: Glu #status predicted

Query Match 100.0%; Score 1171; DB 1; Length 213;
Best Local Similarity 100.0%; Pred. No. 2.4e-80;
Matches 213; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MFKEKQFLVGLSAAALMSISLFSATASASTDYQNWNTDGGGINVAVNGSGNYSVWNSN 60
Db 1 MFKEKQFLVGLSAAALMSISLFSATASASTDYQNWNTDGGGINVAVNGSGNYSVWNSN 60
Qy 61 TGNFVVGKGTGSPFRITINYNAGVWAPNGNGYLTLYGWTSPLEIYYVVDVSWGTYRPTG 120
Db 61 TGNFVVGKGTGSPFRITINYNAGVWAPNGNGYLTLYGWTSPLEIYYVVDVSWGTYRPTG 120
Qy 121 TYGTVKSDGTYDIYITTRYNAPSIDGRTTFTQYWSVRSQKPTGNSNATITFSNHVNA 180
Db 121 TYGTVKSDGTYDIYITTRYNAPSIDGRTTFTQYWSVRSQKPTGNSNATITFSNHVNA 180
Qy 181 WKSHGMNLGSNWAYQVMATGEGYQSSGSSNVTVW 213
Db 181 WKSHGMNLGSNWAYQVMATGEGYQSSGSSNVTVW 213

Query Match 100.0%; Score 1171; DB 1; Length 213;
Best Local Similarity 100.0%; Pred. No. 2.4e-80;
Matches 213; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MFKEKQFLVGLSAAALMSISLFSATASASTDYQNWNTDGGGINVAVNGSGNYSVWNSN 60
Db 1 MFKEKQFLVGLSAAALMSISLFSATASASTDYQNWNTDGGGINVAVNGSGNYSVWNSN 60

Qy 61 TGNFVVGKGTGSPFRITINYNAGVWAPNGNGYLTLYGWTSPLEIYYVVDVSWGTYRPTG 120
Db 61 TGNFVVGKGTGSPFRITINYNAGVWAPNGNGYLTLYGWTSPLEIYYVVDVSWGTYRPTG 120
Qy 121 TYGTVKSDGTYDIYITTRYNAPSIDGRTTFTQYWSVRSQKPTGNSNATITFSNHVNA 180
Db 121 TYGTVKSDGTYDIYITTRYNAPSIDGRTTFTQYWSVRSQKPTGNSNATITFSNHVNA 180
Qy 181 WKSHGMNLGSNWAYQVMATGEGYQSSGSSNVTVW 213
Db 181 WKSHGMNLGSNWAYQVMATGEGYQSSGSSNVTVW 213

RESULT 2
S01734
endo-1,4-beta-xylanase (BC 3.2.1.8) A precursor (validated) - *Bacillus circulans*
N:Alternate names: xylanase A
C:Species: *Bacillus circulans*
C:Date: 07-Jun-1990 #sequence_revision 22-Nov-1996 #text_change 09-Jul-2004
R:Yang, R.C.A.; MacKenzie, C.R.; Narang, S.A.
Nucleic Acids Res. 16, 7187, 1988
A:Title: Nucleotide sequence of a *Bacillus circulans* xylanase gene.
A:Reference number: S01734; MUID:88303346; PMID:3405767
A:Accession: S01734
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-213 <YAN>
A:Cross-references: UNIPROT:P09850; UNIPARC:UPI0000034D1C; EMBL:X07723; NID:g39462; PIDN
A:Note: part of this sequence, including the amino end of the mature protein, was confir
F:Wakarchuk, W.W.; Campbell, R.L.; Sung, W.L.; Bavoodi, J.; Yaguchi, M.
Protein Sci. 3, 467-475, 1994
A:Title: Mutational and crystallographic analyses of the active site residues of the Bac
A:Reference number: A53181; MUID:94290322; PMID:8019418
A:Contents: annotation; X-ray crystallography, 1.49 angstroms, residues 29-213
R:Campbell, R.L.
submitted to the Brookhaven Protein Data Bank, June 1994
A:Reference number: A52866; PDB:1XNB
A:Contents: annotation; X-ray crystallography, 1.49 angstroms, residues 29-213
C:Genetics:
A:Gene: xlnA

C:Function:
A:Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xylans
A:Pathway: xylan degradation
C:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
C:Keywords: extracellular protein; glycosidase; hydrolase; polysaccharide degradation
F:1-28/Domain: signal sequence #status predicted <SIG>
F:29-213/Product: endo-1,4-beta-xylanase A #status experimental <MAT>
F:31-213/Domain: endo-1,4-beta-xylanase homology <XYL>
F:97,108,140/Binding site: substrate (Tyr, Tyr, Arg) #status experimental
F:106,200/Active site: Glu #status experimental

Query Match 99.7%; Score 1168; DB 1; Length 213;
Best Local Similarity 99.5%; Pred. No. 3.9e-80;
Matches 212; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MFKEKQFLVGLSAAALMSISLFSATASASTDYQNWNTDGGGINVAVNGSGNYSVWNSN 60
Db 1 MFKEKQFLVGLSAAALMSISLFSATASASTDYQNWNTDGGGINVAVNGSGNYSVWNSN 60

Qy 61 TGNFVVGKGTGSPFRITINYNAGVWAPNGNGYLTLYGWTSPLEIYYVVDVSWGTYRPTG 120
Db 61 TGNFVVGKGTGSPFRITINYNAGVWAPNGNGYLTLYGWTSPLEIYYVVDVSWGTYRPTG 120
Qy 121 TYGTVKSDGTYDIYITTRYNAPSIDGRTTFTQYWSVRSQKPTGNSNATITFSNHVNA 180
Db 121 TYGTVKSDGTYDIYITTRYNAPSIDGRTTFTQYWSVRSQKPTGNSNATITFSNHVNA 180
Qy 181 WKSHGMNLGSNWAYQVMATGEGYQSSGSSNVTVW 213
Db 181 WKSHGMNLGSNWAYQVMATGEGYQSSGSSNVTVW 213

RESULT 3
S48126
endo-1,4-beta-xylanase (BC 3.2.1.8) S precursor - *Bacillus* sp. (strain YA-14)
N:Alternate names: xylanase S
C:Species: *Bacillus* sp.
A:Variety: strain YA-14
C:Date: 14-Jul-1995 #sequence_revision 22-Nov-1996 #text_change 09-Jul-2004
C:Accession: S48126
R:Ju-Hyun, Y.; Park, Y.S.; Yum, D.Y.; Kim, J.M.; Kong, I.S.; Bai, D.H.
J. Microbiol. Biotechnol. 3, 139-145, 1993
A:Title: Nucleotide sequence and analysis of a xylanase gene (xyns) from alkali-tolerant
A:Reference number: S48126
A:Accession: S48126
A:Molecule type: DNA
A:Residues: 1-213 <JUH>
A:Cross-references: UNIPROT:Q59256; UNIPARC:UPI0000060D47; EMBL:X59058; NID:g458800; PID
A:Experimental source: strain YA-14
C:Genetics:
A:Gene: xynS
C:Function:
A:Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xylans
A:Pathway: xylan degradation
C:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
C:Keywords: extracellular protein; glycosidase; hydrolase; polysaccharide degradation
F:1-28/Domain: signal sequence #status predicted <SIG>
F:29-213/Product: endo-1,4-beta-xylanase S #status predicted <MAT>
F:31-213/Domain: endo-1,4-beta-xylanase homology <XYL>
F:106,200/Active site: Glu #status predicted

Query Match 99.5%; Score 1165; DB 1; Length 213;
Best Local Similarity 99.1%; Pred. No. 6.6e-80;
Matches 211; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MFKEKQFLVGLSAAALMSISLFSATASASTDYQNWNTDGGGINVAVNGSGNYSVWNSN 60
Db 1 MFKEKQFLVGLSAAALMSISLFSATASASTDYQNWNTDGGGINVAVNGSGNYSVWNSN 60

Qy 61 TGNFVVGKGTGSPFRITINYNAGVWAPNGNGYLTLYGWTSPLEIYYVVDVSWGTYRPTG 120
Db 61 TGNFVVGKGTGSPFRITINYNAGVWAPNGNGYLTLYGWTSPLEIYYVVDVSWGTYRPTG 120

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 3, 2006, 09:08:23 ; Search time 42 Seconds
(without alignments)
487.956 Million cell updates/sec

Title: US-10-626-724-5

Perfect score: 1171

Sequence: 1 MFKPKNVLGLSAAALMSIS.....YQNWATEGYSGSSNVTVM 213

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_80.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1171	100.0	213	1	I40569
2	1168	99.7	213	1	S01734
3	1165	99.5	213	1	S48126
4	864.5	73.8	210	2	C83762
5	651.5	55.6	241	2	T37005
6	637	54.4	240	1	J30591
7	621	53.0	240	1	S47512
8	609.5	52.0	644	1	I40712
9	600	51.2	225	1	S57477
10	594	50.7	333	1	J50590
11	594	50.7	332	2	T50601
12	578	49.4	235	2	JC7577
13	577	49.3	221	1	S57469
14	552	47.1	227	2	S43919
15	540	46.1	219	2	S71472
16	530	45.3	197	1	A44597
17	525	44.8	221	2	JC7307
18	523	44.7	190	1	A44595
19	515.5	44.0	241	2	S71473
20	513	43.8	190	1	A44593
21	506	43.2	190	1	A44594
22	505	43.1	223	2	S39883
23	503	43.0	222	2	S39154
24	480.5	41.0	354	1	S51779
25	469	40.1	661	1	S59633
26	461.5	39.4	228	1	WBESXP
27	436	37.2	656	1	S59631
28	420	35.9	261	1	S12745
29	409	34.9	511	1	JQ1935

30 405 34.6 229 2 S39155 xylanase 2 - fungus
31 388 33.1 954 1 S20907 endo-1,4-beta-xyla
32 382.5 32.7 211 1 JC1198 endo-1,4-beta-xyla
33 381 32.5 211 1 S48229 endo-1,4-beta-xyla
34 377 32.2 789 2 S58235 endo-1,4-beta-xyla
35 375 32.0 211 2 S49542 endo-1,4-beta-xyla
36 361 30.8 209 2 JC4909 endo-1,4-beta-xyla
37 349.5 29.8 781 2 S51592 XynB precursor - R
38 336.5 28.7 602 2 A36910 xylanase, beta(1,3
39 271.5 23.2 807 2 S24754 endo-1,4-beta-xyla
40 264.5 22.6 607 2 S49528 endoxylanase - rum
41 262 22.4 608 2 B53295 xylanase (EC 3.2.1
42 245 20.9 266 1 S48865 endo-1,4-beta-xyla
43 133 11.4 313 2 T04776 hypothetical prote
44 126 10.8 50 2 A61149 endo-1,4-beta-xyla
45 120 10.2 666 2 A42296 lysozyme 2 (EC 3.2

ALIGNMENTS

RESULT 1

I40569

endo-1,4-beta-xylanase (EC 3.2.1.8) A precursor - Bacillus subtilis

Alternate names: xylanase A

C:Species: Bacillus subtilis

C:Date: 12-Aug-1996 #sequence revision 02-Jul-1998 #text change 09-Jul-2004

C:Accession: I40569; S39157; S39158; A53635; F69735; S51711

R:Wolf, M.; Geczi, A.; Simon, O.; Borriass, R.

Microbiology 141, 281-290, 1995

A:Title: Genes encoding xylan and beta-glucan hydrolysing enzymes in Bacillus subtilis:

A:Reference number: I40370; MUID:95219081; PMID:7704256

A:Accession: I40569

A:Status: nucleic acid sequence not shown; translation not shown; translated from GB/EME

A:Molecule type: DNA

A:Residues: 1-22, P', 24-213 <WOL>

A:Cross-references: UNIPROT:P18429; UNIPARC:UPI000000B63D0; EMBL:Z34519; NID:G2995396; P1

A:Experimental source: strain 168

R:Paice, M.G.; Bourbonnais, R.; Desrochers, M.; Jurasek, L.; Yaguchi, M.

Arch. Microbiol. 144, 201-206, 1986

A:Title: A xylanase gene from Bacillus subtilis: nucleotide sequence and comparison with

A:Reference number: S39157

A:Accession: S39157

A:Molecule type: DNA

A:Residues: 1-213 <PA11>

A:Cross-references: UNIPARC:UPI00000336C9; EMBL:M36648; NID:G143842; PIDN:AAA22897.1; P1

A:Experimental source: strain PAP115

A:Accession: S39158

A:Molecule type: protein

A:Residues: 29-58;60-73;75-76 <PA12>

A:Cross-references: UNIPARC:UPI000015759E; UNIPARC:UPI0000172962; UNIPARC:UPI0000172963

A:Experimental source: strain PAP115

R:Miao, S.; Ziser, L.; Rebersold, R.; Withers, S.G.

Biochemistry 33, 7027-7032, 1994

A:Title: Identification of glutamic acid 78 as the active site nucleophile in Bacillus s

A:Reference number: A53635; MUID:94271752; PMID:7911679

A:Accession: A53635

A:Status: preliminary

A:Molecule type: protein

A:Residues: 97-107 <MIA>

A:Cross-references: UNIPARC:UPI0000172964

R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter

C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho

A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.

Nature 390, 249-256, 1997

A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler

iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.

Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,

A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel

Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle

Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,

A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror

akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpatra, P.; Tognoni, A.; Tosato, V.; Uchiyama,

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QY 121 TYKGTVKSDGGTYDYITTRYNAPSIDGDRITFTQVWSVRQSKRPTGNSNATITFSNHVNA 180
Db 121 TYKGTVKSDGGTYDYITTRYNAPSIDGDRITFTQVWSVRQSKRPTGNSNATITFSNHVNA 180

QY 181 WKSHGMNLGNNWAYQVMATEGYQSSGSSNVTVM 213
Db 181 WKSHGMNLGNNWAYQVLATEGYQSSGSSNVTVM 213

RESULT 4
C83762
endo-1,4-beta-xylanhydrolase BH0899 [imported] - Bacillus halodurans (strain C-125)
C:Species: Bacillus halodurans
C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C:Accession: C83762
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A:Reference number: A83650; MUID:20512582; PMID:11058132
A:Accession: C83762
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-210 <STO>
A:Cross-references: UNIPROT:Q9KEP3; UNIPARC:UPI00000DCBD1; GB:AP001510; GB:BA000004; NID
A:Experimental source: strain C-125
C:Genetics:
A:Gene: BH0899
C:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology

Query Match 73.8%; Score 864.5; DB 2; Length 210;
Best Local Similarity 74.2%; Pred. No. 1.6e-57;
Matches 158; Conservative 19; Mismatches 33; Indels 3; Gaps 2;

QY 1 MFKFKKFLVGLSALMSISLFSATASASTDYQWNTDGGGIVNAVNGSN 60
Db 1 MFKFTVKLVTVVIATISFCLSAVPASA--NTYWQYTDGGTVNATNGPGGNSYVTRD 58

QY 61 TGNFVVGKWTGSPRTTINYNAGVWAPNGNGYLYLTYGTRSPLEIYYVDSWGYRPTG 120
Db 59 TGNFVVGKWEIGSPRTTHYNAGVWEPGNGYLYLTYGTRNQLIEYYVVDNMGYRPTG 118

QY 121 TYKGTVKSDGGTYDYITTRYNAPSIDGDRITFTQVWSVRQSKRPTGNSNATITFSNHVNA 180
Db 119 THRGTVVSDGGTYDYITTRYNAPSIDGTQ--TFQQFWSVRQSKRPTGNVNSITFSNHVNA 177

QY 181 WKSHGMNLGNNWAYQVMATEGYQSSGSSNVTVM 213
Db 178 WENAGMNLGSSWSYQVLATEGYQSSGSSNVTVM 210

RESULT 5
T37005
endo-1,4-beta-xylanase - Streptomyces coelicolor
C:Species: Streptomyces coelicolor
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T37005
R:Oliver, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, August 1999
A:Reference number: Z21618
A:Accession: T37005
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-241 <OLI>
A:Cross-references: UNIPROT:Q9RI72; UNIPARC:UPI00000DB349; EMBL:AL109949; PIDN:CAB52919.
A:Experimental source: strain A3(2)
C:Genetics:
A:Gene: xinc; SCOEDB:SCU11.34c
C:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology

Query Match 55.6%; Score 651.5; DB 2; Length 241;
Best Local Similarity 58.4%; Pred. No. 1.3e-41;
Matches 129; Conservative 25; Mismatches 50; Indels 17; Gaps 6;
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QY 5 KKNFLVG--LSAALMSISLFSATASAST-----DYQWNTDGGGIVNAVNGSG 51
Db 23 RRGFLGGAGTALATASGLLLPGTAHAATTTTNGTGDGMYSFTWTDGGGVSMTLNGG 82

QY 52 GNYSVNWSNTGNFVVGKWTGSPRTTINYNAGVWAPNGNGYLYLTYGTRSPLEIYYVD 111
Db 83 GSYSTQWNTNCGNFVAGKCGWSTGGR--RTVRYN--GYFNPNGNGYGLYGMTSNPLVEIYVD 140

QY 112 SWGYRPTGTYKGTVKSDGGTYDYITTRYNAPSIDGDRITFTQVWSVRQSKRPTGNSNAT 171
Db 141 NMGYSYRPTGTYKGTVKSDGGTYDYITTRYNAPSVEGTK--TFQQYWSVRQSKVTSGS--GT 198

QY 172 ITFNSHNVAWSHGNNLGNWAYQVMATEGYQSSGSSNVTVM 212
Db 199 ITTGNHFDPAWARAGNMCGFRYYMIMATEGYQSSGSSNITV 239

RESULT 6
J50591
endo-1,4-beta-xylanase (EC 3.2.1.8) C precursor - Streptomyces lividans
N:Alternate names: xylanase C
C:Species: Streptomyces lividans
C:Date: 14-Jul-1994 #sequence_revision 22-Nov-1996 #text_change 09-Jul-2004
C:Accession: J50591; PS0240
R:Shareck, F.; Roy, C.; Yaguchi, M.; Morosoli, R.; Kluepfel, D.
Gene 107, 75-82, 1991
A:Title: Sequences of three genes specifying xylanases in Streptomyces lividans.
A:Reference number: J50589; MUID:92077439; PMID:1743521
A:Accession: J50591
A:Molecule type: DNA
A:Residues: 1-240 <SHA>
A:Cross-references: UNIPROT:P26220; UNIPARC:UPI0000034D31; GB:M64553; NID:G153530; PIDN
A:Accession: J50591
A:Molecule type: protein
A:Residues: 50-80 <SH2>
A:Cross-references: UNIPARC:UPI00000172965
C:Genetics:
A:Gene: xinc
C:Function:
A:Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xylans
A:Pathway: xylan degradation
C:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
C:Keywords: extracellular protein; glycosidase; hydrolase; polysaccharide degradation
F:1-49/Domain: signal sequence #status predicted <SIG>
F:50-240/Product: endo-1,4-beta-xylanase C #status experimental <NAT>
F:62-239/Domain: endo-1,4-beta-xylanase homology <XYL>
F:134,226/Active site: Glu #status predicted

Query Match 54.4%; Score 637; DB 1; Length 240;
Best Local Similarity 57.5%; Pred. No. 1.6e-40;
Matches 127; Conservative 24; Mismatches 52; Indels 18; Gaps 6;

QY 5 KKNFLVG--LSAALMSISLFSATASAST-----DYQWNTDGGGIVNAVNGSG 51
Db 23 RRGFLGGAGTALATASGLLLPGTAHAATTTTNGTGDGMYSFTWTDGGGVSMTLNGG 82

QY 52 GNYSVNWSNTGNFVVGKWTGSPRTTINYNAGVWAPNGNGYLYLTYGTRSPLEIYYVD 111
Db 83 GSYSTQWNTNCGNFVAGKCGWSTGD--GNVRYN--GYFNPNGNGYGLYGMTSNPLVEIYVD 139

QY 112 SWGYRPTGTYKGTVKSDGGTYDYITTRYNAPSIDGDRITFTQVWSVRQSKRPTGNSNAT 171
Db 140 NMGYSYRPTGTYKGTVKSDGGTYDYITTRYNAPSVEGTK--TFQQYWSVRQSKVTSGS--GT 197

QY 172 ITFNSHNVAWSHGNNLGNWAYQVMATEGYQSSGSSNVTVM 212
Db 198 ITTGNHFDPAWARAGNMCGFRYYMIMATEGYQSSGSSNITV 238

RESULT 7
S47512
endo-1,4-beta-xylanase (EC 3.2.1.8) precursor - Streptomyces sp.
N:Alternate names: xylanase
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C;Date: 10-Mar-1994 #sequence_revision 22-Nov-1996 #text_change 26-Feb-1999

C;Accession: J50590; PS0239

R;Shareck, F.; Roy, C.; Yaguchi, M.; Morosoli, R.; Kluepfel, D.

Gene 107, 75-82, 1991

A;Title: Sequences of three genes specifying xylanases in Streptomyces lividans.

A;Reference number: J50589; MUID:92077439; PMID:1743521

A;Accession: J50590

A;Molecule type: DNA

A;Residues: 1-333 <SHA>

A;Cross-references: UNIPARC:UPI000017296A; GB:M64552

A;Accession: PS0239

A;Molecule type: protein

A;Residues: 41-71 <SH2>

A;Cross-references: UNIPARC:UPI000017296B

C;Genetics:

A;Gene: xlnB

C;Function:

A;Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xylans

A;Pathway: xylan degradation

C;Superfamily: Clostridium endo-1,4-beta-xylanase B; endo-1,4-beta-xylanase homology

C;Keywords: extracellular protein; glycosidase; hydrolase; polysaccharide degradation

F;1-40/Domain: signal sequence #status predicted <SIG>

F;41-333/Product: endo-1,4-beta-xylanase B #status experimental <MAT>

F;54-230/Domain: endo-1,4-beta-xylanase homology <XVL>

F;127,217/Active site: Glu #status predicted

Query Match 50.7%; Score 594; DB 1; Length 333;

Best Local Similarity 62.2%; Pred. No. 3.6e-37;

Matches 112; Conservative 19; Mismatches 43; Indels 6; Gaps 4;

Qy 33 YWQWTDGGIYVNAVSGGGYVSNWNTGTFVVGKGTGSPRTTINAGVWAPNGNG 92

Db 56 YYSFTDQGTGVSNMGGGGYSTSWRNTGNFVAGKGWANGGR-RTVQY-SGSFNPSPGNA 113

Qy 93 YLTLYGWTSPLEIYVVDVSMGTPTGTGYKGTGKGTVDIYTTTRYNAPSIDGDRTT 152

Db 114 YLYLWTSNPLVYIYVDNMGTPTGTGYKGTGKGTVDIYTTTRYNAPSVEGTR-T 172

Qy 153 FTQYWSVRQSKRPRTGSGNATITFSNHNWAKSHGMNLSNWAYQVMATEGYQSSGSSNVTV 212

Db 173 FDQYWSVRQSKRTGG---TIITGNHFDARAGMPLGNFYSYIMMATEGYQSSGSSINV 229

Qy 173 FDQYWSVRQSKRTGG---TIITGNHFDARAGMPLGNFYSYIMMATEGYQSSGSSINV 229

Qy 173 FDQYWSVRQSKRTGG---TIITGNHFDARAGMPLGNFYSYIMMATEGYQSSGSSINV 229

Qy 173 FDQYWSVRQSKRTGG---TIITGNHFDARAGMPLGNFYSYIMMATEGYQSSGSSINV 229

Qy 173 FDQYWSVRQSKRTGG---TIITGNHFDARAGMPLGNFYSYIMMATEGYQSSGSSINV 229

Qy 173 FDQYWSVRQSKRTGG---TIITGNHFDARAGMPLGNFYSYIMMATEGYQSSGSSINV 229

Qy 173 FDQYWSVRQSKRTGG---TIITGNHFDARAGMPLGNFYSYIMMATEGYQSSGSSINV 229

Qy 173 FDQYWSVRQSKRTGG---TIITGNHFDARAGMPLGNFYSYIMMATEGYQSSGSSINV 229

Qy 173 FDQYWSVRQSKRTGG---TIITGNHFDARAGMPLGNFYSYIMMATEGYQSSGSSINV 229

Qy 173 FDQYWSVRQSKRTGG---TIITGNHFDARAGMPLGNFYSYIMMATEGYQSSGSSINV 229

Qy 173 FDQYWSVRQSKRTGG---TIITGNHFDARAGMPLGNFYSYIMMATEGYQSSGSSINV 229

Qy 173 FDQYWSVRQSKRTGG---TIITGNHFDARAGMPLGNFYSYIMMATEGYQSSGSSINV 229

Qy 173 FDQYWSVRQSKRTGG---TIITGNHFDARAGMPLGNFYSYIMMATEGYQSSGSSINV 229

Qy 173 FDQYWSVRQSKRTGG---TIITGNHFDARAGMPLGNFYSYIMMATEGYQSSGSSINV 229

Qy 173 FDQYWSVRQSKRTGG---TIITGNHFDARAGMPLGNFYSYIMMATEGYQSSGSSINV 229

Qy 173 FDQYWSVRQSKRTGG---TIITGNHFDARAGMPLGNFYSYIMMATEGYQSSGSSINV 229

Qy 173 FDQYWSVRQSKRTGG---TIITGNHFDARAGMPLGNFYSYIMMATEGYQSSGSSINV 229

Qy 173 FDQYWSVRQSKRTGG---TIITGNHFDARAGMPLGNFYSYIMMATEGYQSSGSSINV 229

Qy 173 FDQYWSVRQSKRTGG---TIITGNHFDARAGMPLGNFYSYIMMATEGYQSSGSSINV 229

Qy 173 FDQYWSVRQSKRTGG---TIITGNHFDARAGMPLGNFYSYIMMATEGYQSSGSSINV 229

Qy 173 FDQYWSVRQSKRTGG---TIITGNHFDARAGMPLGNFYSYIMMATEGYQSSGSSINV 229

Qy 173 FDQYWSVRQSKRTGG---TIITGNHFDARAGMPLGNFYSYIMMATEGYQSSGSSINV 229

Qy 93 YLTLYGWTSPLEIYVVDVSMGTPTGTGYKGTGKGTVDIYTTTRYNAPSIDGDRTT 152

Db 115 YLYLWTSNPLVYIYVDNMGTPTGTGYKGTGKGTVDIYTTTRYNAPSVEGTR-T 173

Qy 153 FTQYWSVRQSKRPRTGSGNATITFSNHNWAKSHGMNLSNWAYQVMATEGYQSSGSSNVTV 212

Db 174 FDQYWSVRQAKRTGG---TIITGNHFDARAGMPLGNFYSYIMMATEGYQSSGSSINV 230

Db 174 FDQYWSVRQAKRTGG---TIITGNHFDARAGMPLGNFYSYIMMATEGYQSSGSSINV 230

Db 174 FDQYWSVRQAKRTGG---TIITGNHFDARAGMPLGNFYSYIMMATEGYQSSGSSINV 230

Db 174 FDQYWSVRQAKRTGG---TIITGNHFDARAGMPLGNFYSYIMMATEGYQSSGSSINV 230

Db 174 FDQYWSVRQAKRTGG---TIITGNHFDARAGMPLGNFYSYIMMATEGYQSSGSSINV 230

Db 174 FDQYWSVRQAKRTGG---TIITGNHFDARAGMPLGNFYSYIMMATEGYQSSGSSINV 230

Db 174 FDQYWSVRQAKRTGG---TIITGNHFDARAGMPLGNFYSYIMMATEGYQSSGSSINV 230

Db 174 FDQYWSVRQAKRTGG---TIITGNHFDARAGMPLGNFYSYIMMATEGYQSSGSSINV 230

Db 174 FDQYWSVRQAKRTGG---TIITGNHFDARAGMPLGNFYSYIMMATEGYQSSGSSINV 230

Db 174 FDQYWSVRQAKRTGG---TIITGNHFDARAGMPLGNFYSYIMMATEGYQSSGSSINV 230

Db 174 FDQYWSVRQAKRTGG---TIITGNHFDARAGMPLGNFYSYIMMATEGYQSSGSSINV 230

Db 174 FDQYWSVRQAKRTGG---TIITGNHFDARAGMPLGNFYSYIMMATEGYQSSGSSINV 230

Db 174 FDQYWSVRQAKRTGG---TIITGNHFDARAGMPLGNFYSYIMMATEGYQSSGSSINV 230

Db 174 FDQYWSVRQAKRTGG---TIITGNHFDARAGMPLGNFYSYIMMATEGYQSSGSSINV 230

Db 174 FDQYWSVRQAKRTGG---TIITGNHFDARAGMPLGNFYSYIMMATEGYQSSGSSINV 230

Db 174 FDQYWSVRQAKRTGG---TIITGNHFDARAGMPLGNFYSYIMMATEGYQSSGSSINV 230

Db 174 FDQYWSVRQAKRTGG---TIITGNHFDARAGMPLGNFYSYIMMATEGYQSSGSSINV 230

Db 174 FDQYWSVRQAKRTGG---TIITGNHFDARAGMPLGNFYSYIMMATEGYQSSGSSINV 230

Db 174 FDQYWSVRQAKRTGG---TIITGNHFDARAGMPLGNFYSYIMMATEGYQSSGSSINV 230

Db 174 FDQYWSVRQAKRTGG---TIITGNHFDARAGMPLGNFYSYIMMATEGYQSSGSSINV 230

Db 174 FDQYWSVRQAKRTGG---TIITGNHFDARAGMPLGNFYSYIMMATEGYQSSGSSINV 230

Db 174 FDQYWSVRQAKRTGG---TIITGNHFDARAGMPLGNFYSYIMMATEGYQSSGSSINV 230

Db 174 FDQYWSVRQAKRTGG---TIITGNHFDARAGMPLGNFYSYIMMATEGYQSSGSSINV 230

Db 174 FDQYWSVRQAKRTGG---TIITGNHFDARAGMPLGNFYSYIMMATEGYQSSGSSINV 230

Db 174 FDQYWSVRQAKRTGG---TIITGNHFDARAGMPLGNFYSYIMMATEGYQSSGSSINV 230

Db 174 FDQYWSVRQAKRTGG---TIITGNHFDARAGMPLGNFYSYIMMATEGYQSSGSSINV 230

Db 174 FDQYWSVRQAKRTGG---TIITGNHFDARAGMPLGNFYSYIMMATEGYQSSGSSINV 230

Db 174 FDQYWSVRQAKRTGG---TIITGNHFDARAGMPLGNFYSYIMMATEGYQSSGSSINV 230

Db 174 FDQYWSVRQAKRTGG---TIITGNHFDARAGMPLGNFYSYIMMATEGYQSSGSSINV 230

Db 174 FDQYWSVRQAKRTGG---TIITGNHFDARAGMPLGNFYSYIMMATEGYQSSGSSINV 230

Db 174 FDQYWSVRQAKRTGG---TIITGNHFDARAGMPLGNFYSYIMMATEGYQSSGSSINV 230

Db 174 FDQYWSVRQAKRTGG---TIITGNHFDARAGMPLGNFYSYIMMATEGYQSSGSSINV 230

Db 174 FDQYWSVRQAKRTGG---TIITGNHFDARAGMPLGNFYSYIMMATEGYQSSGSSINV 230

Db 174 FDQYWSVRQAKRTGG---TIITGNHFDARAGMPLGNFYSYIMMATEGYQSSGSSINV 230

Db 174 FDQYWSVRQAKRTGG---TIITGNHFDARAGMPLGNFYSYIMMATEGYQSSGSSINV 230

Db 174 FDQYWSVRQAKRTGG---TIITGNHFDARAGMPLGNFYSYIMMATEGYQSSGSSINV 230

Db 174 FDQYWSVRQAKRTGG---TIITGNHFDARAGMPLGNFYSYIMMATEGYQSSGSSINV 230

Db 174 FDQYWSVRQAKRTGG---TIITGNHFDARAGMPLGNFYSYIMMATEGYQSSGSSINV 230

Db 174 FDQYWSVRQAKRTGG---TIITGNHFDARAGMPLGNFYSYIMMATEGYQSSGSSINV 230

Db 174 FDQYWSVRQAKRTGG---TIITGNHFDARAGMPLGNFYSYIMMATEGYQSSGSSINV 230

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 3, 2006, 09:04:18 ; Search time 199 Seconds
(without alignment)
470.290 Million cell updates/sec

Title: US-10-626-724-5

Perfect score: 1171

Sequence: 1 MFKPKNPLVLGLSALMSIS.....YQVMATEGYQSSGSNTVTW 213

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_21:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*
- 9: Geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1171	100.0	213	3	Aay93752 A bacteri
2	1171	100.0	213	7	Adc27541 Bacillus
3	1171	100.0	213	7	Ado55909 Bacillus
4	1171	100.0	213	8	Adj34972 Xylanase
5	1168	99.7	213	3	Aab48532 Bacillus
6	1168	99.7	213	3	Aab48518 Bacillus
7	1168	99.7	213	5	Aao18638 B subtili
8	1168	99.7	213	5	Aao18624 Endo-1,4-
9	1168	99.7	213	8	Adj35008 Xylanase
10	1168	99.7	213	8	Adi66728 B. circul
11	1168	99.7	213	8	Adi66740 B. subtil
12	1161	99.1	213	3	Aay93755 A bacteri
13	1154	98.5	213	3	Aay93753 A bacteri
14	1149	98.1	213	3	Aay93754 A bacteri
15	1130	96.5	213	2	Aar47200 Modified
16	1130	96.5	213	3	Aay93751 A Bacteri
17	1125	96.1	213	8	Ado70164 Xylanase,
18	1104	94.3	213	8	Adj35014 Xylanase
19	1097	93.7	213	8	Adj35086 Xylanase
20	1041	88.9	185	2	Aaw60732 Xylanase
21	1041	88.9	185	3	Aay98064 B. subtil
22	1041	88.9	185	3	Aab69043 B. subtil
23	1041	88.9	185	4	Aau07391 Bacillus
24	1041	88.9	185	5	Aae18441 Bacillus

25	1041	88.9	185	7	Adc27530 Bacillus
26	1041	88.9	197	8	Adh10230 Xylanase
27	1041	88.9	353	4	Aab69045 Xylanase
28	1041	88.9	360	8	Adh10231 Xylanase-
29	1038	88.6	185	2	Aaw60730 Xylanase
30	1038	88.6	185	3	Aay98062 B. circul
31	1038	88.6	185	5	Aao18625 B. circul
32	1038	88.6	185	5	Aae18439 Bacillus
33	1034	88.3	353	4	Aab69046 NL-xylana
34	1033	88.2	185	2	Aaw60279 Modified
35	1030	88.0	185	2	Aaw60278 Modified
36	987	84.3	185	3	Aab48524 Xylanase
37	987	84.3	185	3	Aab48523 Xylanase
38	987	84.3	185	5	Aao18629 Modified
39	987	84.3	185	5	Aao18630 Modified
40	987	84.3	185	8	Adi66732 B. circul
41	984	84.0	185	3	Aab48528 Xylanase
42	984	84.0	185	5	Aao18634 Modified
43	984	84.0	185	8	Adi66736 B. circul
44	979	83.6	185	3	Aab48526 Xylanase
45	979	83.6	185	5	Aao18632 Modified

ALIGNMENTS

RESULT 1

AAy93752
ID AAY93752 standard; protein; 213 AA.
XX
AC AAY93752;
XX
DT 03-OCT-2000 (first entry)
XX
DE A bacterial endo-beta-1,4-xylanase protein.
XX
KW Endo-beta-1,4-xylanase inhibitor; wheat flour; xylanase; bakery product;
KW dough; dough preparation.
XX
OS Bacillus subtilis.
XX
PN WO200039289-A2.
XX
PD 06-JUL-2000.
XX
PF 17-DEC-1999; 99WO-IB002071.
XX
PR 23-DEC-1998; 98GB-00028599.
PR 06-APR-1999; 99GB-00007805.
PR 15-APR-1999; 99GB-00008645.
(DANI-) DANISCO AS.
XX
SI Sibbesen O, Sorensen JF;
XX
WI WPI; 2000-465744/40.
XX
N-PSDB; AAA47154.
XX
PT Mutant xylanase protein identified using xylanase inhibitor useful for
preparing non-sticky dough for bakery products.
XX
Claim 10; Page 108; 112pp; English.
XX
The present sequence represents an endo-beta-1,4-xylanase. The
specification also describes an endo-beta-1,4-xylanase inhibitor, which
is obtained from wheat flour. The specification also describes a mutant
xylanase protein. The xylanase is useful for preparing a foodstuff,
preferably a bakery product or a substance (e.g. a dough) for making the
bakery product. Wild type xylanase or mutant xylanase is useful for
preparing a dough that is less sticky than a dough comprising a fungal
xylanase. The xylanase inhibitor is useful for screening high degree
resistance xylanases for dough preparation. The xylanase is also useful
for preparing a non-sticky dough. A combination of xylanase and the

CC inhibitor is useful for calibrating and/or determining the quantity of
CC inhibitor in a wheat flour sample
XX
SQ Sequence 213 AA;

Query Match 100.0%; Score 1171; DB 3; Length 213;
Best Local Similarity 100.0%; Pred. No. 1.8e-91;
Matches 213; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFKFKNFLVGLSALMSISLFSATASASTDYQWNTDGGGIYVNAVNGSGNYSVNWSN 60
Db 1 MFKFKNFLVGLSALMSISLFSATASASTDYQWNTDGGGIYVNAVNGSGNYSVNWSN 60
Qy 61 TGNFVVGKGTGSPFTINYNAGVWAPNGNGYLTLYGWTRSPLEIYVVDVDSWGTYRPTG 120
Db 61 TGNFVVGKGTGSPFTINYNAGVWAPNGNGYLTLYGWTRSPLEIYVVDVDSWGTYRPTG 120
Qy 121 TYKGTVKSDDGTYDIYTTTRYNAPSIDGDRITFTQYWSVRSQKPTGSNATITFSNHVNA 180
Db 121 TYKGTVKSDDGTYDIYTTTRYNAPSIDGDRITFTQYWSVRSQKPTGSNATITFSNHVNA 180
Qy 181 WKSHGMNLGSNWAYQVWATEGYQSSGSSNVTVM 213
Db 181 WKSHGMNLGSNWAYQVWATEGYQSSGSSNVTVM 213

RESULT 2
ADC27541
ID ADC27541 standard; protein; 213 AA.
XX
AC ADC27541;
XX
DT 18-DEC-2003 (first entry)
XX
DE Bacillus subtilis wild-type xylanase enzyme.
XX
KW xylanase; xylanase inhibitor; thermosensitivity; plant cell wall;
KW plant material; baking; processing cereal; starch production;
KW processing wood; wood pulp bleaching; animal feed; flour separation;
KW wetmilling; paper and pulp production; flour dough; hemicellulose;
KW arabinoxylan; food supplement; xylan; baking process; bread volume;
KW crumb structure; crumb appearance; shelf-life; enzyme.
XX
OS Bacillus subtilis.
XX
XX WO2003020923-A1.
XX
XX 13-MAR-2003.
XX
XX 30-AUG-2002; 2002WO-IB003797.
XX
PR 04-SEP-2001; 2001GB-00021387.
XX
PA (DANI-) DANISCO AS.
XX
PI Sibbesen O, Sorensen JF;
XX
XX WPI; 2003-332934/31.
DR N-PSDB; ADC27538.
XX
PT Novel variant xylanase polypeptide having altered sensitivity to a
PT xylanase inhibitor and altered thermosensitivity as compared with a
PT parent xylanase enzyme, useful in baking, processing cereals, starch
PT production.
XX
PS Disclosure; Fig 1; 63pp; English.
XX
CC This invention relates to a novel variant xylanase protein or its
CC fragment having xylanase activity. the variants have one or more amino
CC acid modifications so that the protein or fragment has an altered
CC sensitivity to a xylanase inhibitor and has an altered thermosensitivity
CC as compared with a parent xylanase enzyme. The variant xylanases of the
CC invention are useful for degrading or modifying a plant cell wall, and

CC for processing a plant material. They may be useful for baking,
CC processing cereals, starch production, in processing wood, and enhancing
CC the bleaching of wood pulp. They may also be useful for a variety of
CC applications such as animal feed, flour separation (wetmilling) and paper
CC and pulp production. In addition, they may also be useful for preparing a
CC flour dough. The enzymes of the invention may alter or reduce the
CC viscosity derived from the presence of hemicellulose or arabinoxylan in a
CC solution or system comprising plant cell wall material, and for modifying
CC food and/or feed supplement comprising xylan. Use of the variant
CC xylanases in baking processes improves the properties of flour based
CC doughs and products made from the doughs. The baked products have highly
CC desirable characteristics with respect to blood volume, crumb structure
CC and appearance and additionally have an extended shelf-life. The enzymes
CC of the invention have reduced thermosensitivity and inhibitor
CC sensitivity, which allows a reduction in the amount of xylanase required
CC for animal feed, starch production and baking. The present sequence is
CC that of the full-length wild-type Bacillus subtilis xylanase which was
CC used to create the variant xylanases of the invention.

SQ Sequence 213 AA;

Query Match 100.0%; Score 1171; DB 7; Length 213;
Best Local Similarity 100.0%; Pred. No. 1.8e-91;
Matches 213; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFKFKNFLVGLSALMSISLFSATASASTDYQWNTDGGGIYVNAVNGSGNYSVNWSN 60
Db 1 MFKFKNFLVGLSALMSISLFSATASASTDYQWNTDGGGIYVNAVNGSGNYSVNWSN 60
Qy 61 TGNFVVGKGTGSPFTINYNAGVWAPNGNGYLTLYGWTRSPLEIYVVDVDSWGTYRPTG 120
Db 61 TGNFVVGKGTGSPFTINYNAGVWAPNGNGYLTLYGWTRSPLEIYVVDVDSWGTYRPTG 120
Qy 121 TYKGTVKSDDGTYDIYTTTRYNAPSIDGDRITFTQYWSVRSQKPTGSNATITFSNHVNA 180
Db 121 TYKGTVKSDDGTYDIYTTTRYNAPSIDGDRITFTQYWSVRSQKPTGSNATITFSNHVNA 180
Qy 181 WKSHGMNLGSNWAYQVWATEGYQSSGSSNVTVM 213
Db 181 WKSHGMNLGSNWAYQVWATEGYQSSGSSNVTVM 213

RESULT 3

ADO55909
ID ADO55909 standard; protein; 213 AA.

XX
AC ADO55909;

XX
DT 15-JUL-2004 (first entry)

XX
DE Bacillus subtilis xynA protein sequence SeqID4.

XX
KW cellulase; microorganism; organic fertiliser; faeces; urine;
KW domestic animal; sawdust; pLYH7-39; bgIC; xylanase; pLYH8-49; xynA;
KW pLYH8-62; xynD; pectate lyase; pLYH9-24; pella; pLYH9-46; pelB;
KW fermentation; enzyme.

XX
OS Bacillus subtilis.

XX
XX KR2003015943-A.

XX
PN 26-FEB-2003.

XX
PD 18-AUG-2001; 2001KR-00049794.

XX
PF 18-AUG-2001; 2001KR-00049794.

XX
PR (KOBI-) KOREA BIO FERTILIZER CO LTD.

XX
PA Lee YH, Yoon HJ;

XX
XX WPI; 2003-455433/43.

DR
DR N-PSDB; ADO55908.

XX PT Gene encoding cellulase, cellulase expressed by the same, microorganism
 PT containing the same gene, and organic fertilizer using the same
 microorganism.
 XX PT
 XX PS Claim 2; SEQ ID NO 4; lpp; Korean.
 XX PS
 CC This invention relates to novel genes encoding cellulase, cellulase
 CC expressed by the same, a microorganism containing the same gene, and an
 CC organic fertilizer using the same microorganism, therefore the organic
 CC fertilizer can be rapidly produced from a mixture of the faeces and urine
 CC of domestic animals and sawdust. The microorganism *Bacillus subtilis*
 CC contains one cellulase encoding gene pLVH7-39 (bgIC), two xylanase
 CC encoding genes pLVH8-49 (xynA) and pLVH8-62 (xynD) and two pectate lyase
 CC encoding genes pLVH9-24 (pelA) and pLVH9-46 (pelB). The organic fertilizer
 CC is produced by inoculating an appropriate amount of the microorganism
 CC *Bacillus subtilis* into the mixture of the faeces and urine of domestic
 CC animals and sawdust and fermenting the mixture. The present sequence is
 CC that of a *Bacillus subtilis* protein which is related to the production of
 CC the organic fertilizer of the invention.
 XX XX
 SQ Sequence 213 AA;
 Query Match 100.0%; Score 1171; DB 7; Length 213;
 Best Local Similarity 100.0%; Pred. No. 1.8e-91;
 Matches 213; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MFKEKKNFLVGLSALMSISLFSATASAASDYQNWNTDGGGIYVNAVSGSGNYSVNWSN 60
 Db 1 MFKEKKNFLVGLSALMSISLFSATASAASDYQNWNTDGGGIYVNAVSGSGNYSVNWSN 60
 Qy 61 TGNFVVGKGTGSPFRITINYNAGVWAPNGNGYLTLYGWTRSPLEIYYVVDVDSWGTYPRTG 120
 Db 61 TGNFVVGKGTGSPFRITINYNAGVWAPNGNGYLTLYGWTRSPLEIYYVVDVDSWGTYPRTG 120
 Qy 121 TYKGTVKSDDGTYDIYTTTRYNAPSIDGDRFTFTQYWSVRSKRPTGNSNATITFSNHVNA 180
 Db 121 TYKGTVKSDDGTYDIYTTTRYNAPSIDGDRFTFTQYWSVRSKRPTGNSNATITFSNHVNA 180
 Qy 181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTW 213
 Db 181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTW 213
 RESULT 4
 ADJ34972
 ID ADJ34972 standard; protein; 213 AA.
 AC ADJ34972;
 XX XX
 XX DT 22-APR-2004 (first entry)
 XX DE Xylanase from an environmental sample seq id 188.
 XX KW antibacterial; fungicide; thermostable xylanase activity;
 KW dough conditioning; beverage production; nutritional supplement;
 KW animal feed; lignin reduction; wood product; xylan; bacterial infection;
 KW fungal infection; coccidiosis.
 XX XX
 OS Unidentified.
 XX XX
 XX FN WO2003106654-A2.
 XX XX
 XX PD 24-DEC-2003.
 XX XX
 XX PF 16-JUN-2003; 2003WO-US019153.
 XX XX
 XX PR 14-JUN-2002; 2002US-0389299P.
 XX XX
 XX PA (DIVE-) DIVERSA CORP.
 XX XX
 XX PI Steer B, Callen W, Healey S, Hazlewood G, Wu D, Blum D;
 PI Esteghlalian A;

XX WPI; 2004-099016/10.
 DR N-PSDB; ADJ34971.
 XX PT
 XX PT Novel xylanase recombinant polypeptide useful for improving textile
 texture, treating paper, eliminating microorganisms.
 XX PS
 XX PS Claim 60; SEQ ID NO 188; 570pp; English.
 XX PS
 CC The invention describes an isolated or recombinant polypeptide (I),
 CC having 50% or more identity to 190 300-1200 residue amino acid sequences
 CC (SI), given in the specification, over a region of 100 or more residues
 CC and the polypeptide as thermostable xylanase activity. (I) is useful for:
 CC dough conditioning; beverage production; as a nutritional supplement in
 CC animal feed; reducing lignin in a wood or a wood product; and for
 CC eliminating and protecting animals from a microorganism comprising xylan.
 CC The polynucleotide (II) encoding (I) is useful for amplifying nucleic
 CC acid encoding a polypeptide having a xylanase activity which involves
 CC amplification of a template nucleic acid with a primer pair capable of
 CC amplifying (II) or its subsequence. (I) is useful for treating and
 CC preventing bacterial infection and fungal infection e.g. coccidiosis.
 CC This is the amino acid sequence of a xylanase protein isolated from an
 CC environmental sample.
 XX XX
 SQ Sequence 213 AA;
 Query Match 100.0%; Score 1171; DB 8; Length 213;
 Best Local Similarity 100.0%; Pred. No. 1.8e-91;
 Matches 213; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MFKEKKNFLVGLSALMSISLFSATASAASDYQNWNTDGGGIYVNAVSGSGNYSVNWSN 60
 Db 1 MFKEKKNFLVGLSALMSISLFSATASAASDYQNWNTDGGGIYVNAVSGSGNYSVNWSN 60
 Qy 61 TGNFVVGKGTGSPFRITINYNAGVWAPNGNGYLTLYGWTRSPLEIYYVVDVDSWGTYPRTG 120
 Db 61 TGNFVVGKGTGSPFRITINYNAGVWAPNGNGYLTLYGWTRSPLEIYYVVDVDSWGTYPRTG 120
 Qy 121 TYKGTVKSDDGTYDIYTTTRYNAPSIDGDRFTFTQYWSVRSKRPTGNSNATITFSNHVNA 180
 Db 121 TYKGTVKSDDGTYDIYTTTRYNAPSIDGDRFTFTQYWSVRSKRPTGNSNATITFSNHVNA 180
 Qy 181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTW 213
 Db 181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTW 213
 RESULT 5
 AAB48532
 ID AAB48532 standard; protein; 213 AA.
 XX XX
 XX AC AAB48532;
 XX XX
 XX DT 05-MAR-2001 (first entry)
 XX DE *Bacillus subtilis* xylanase.
 XX KW Bacterial; *Bacillus circulans*; xylanase; xylanase activity; XA;
 KW bleaching agent.
 XX OS *Bacillus subtilis*.
 XX XX
 XX FN WO200068396-A2.
 XX XX
 XX PD 16-NOV-2000.
 XX XX
 XX PF 12-MAY-2000; 2000WO-US013172.
 XX XX
 XX PR 12-MAY-1999; 99US-0133714P.
 XX XX
 XX PA (XENC-) XENCOR INC.
 XX XX
 XX PI Bentzien JM;

XX WPI; 2000-679800/66.
XX Non naturally occurring XA protein with enhanced thermophilicity,
PT alkalophilicity or thermostability relative to the naturally occurring
PT Bacillus circulans xylanase is used in an agent for bleaching pulp.
XX
XX
PS Disclosure; Fig 16A; 114pp; English.
XX
CC The present sequence is given in a specification relating to non
CC naturally occurring xylanase activity (XA) proteins. The XA proteins
CC comprise an amino acid sequence less than 97% identical to a naturally
CC occurring Bacillus circulans xylanase. They are modified to exhibit
CC enhanced thermophilicity, alkalophilicity or thermostability relative to
CC the naturally occurring B. circulans xylanase. They may be used as the
CC active compound in a bleaching agent which is used for bleaching pulp
XX
SQ Sequence 213 AA;
Query Match 99.7%; Score 1168; DB 3; Length 213;
Best Local Similarity 99.5%; Pred. No. 3.3e-91;
Matches 212; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MFKEKQFLVGLSAALMSISLFSATASASTDYQNQNTDGGGIYNAVNGSGGYSVNVNSN 60
Db 1 MFKEKQFLVGLSAALMSISLFSATASASTDYQNQNTDGGGIYNAVNGSGGYSVNVNSN 60
Qy 61 TGNFVVGKGTGSPFRTINYNAGVWAPNGNGYLTLYGWTRSPLEIYYVVDVDSWGTYRPTG 120
Db 61 TGNFVVGKGTGSPFRTINYNAGVWAPNGNGYLTLYGWTRSPLEIYYVVDVDSWGTYRPTG 120
Qy 121 TYKGTVKS DGGTYDIYITTRYNAPSIDGDRITFTQYWSVRQSKRPTGSNATITFTNHVNA 180
Db 121 TYKGTVKS DGGTYDIYITTRYNAPSIDGDRITFTQYWSVRQSKRPTGSNATITFTNHVNA 180
Qy 181 WKSHGMNLGSNWAYQVNWATEGYQSSGSSNVTW 213
Db 181 WKSHGMNLGSNWAYQVNWATEGYQSSGSSNVTW 213
RESULT 7
AA018638
ID AA018638 standard; protein; 213 AA.
XX AC AA018638;
XX DT 24-OCT-2002 (first entry)
XX DE B subtilis xylanase.
XX KW Xylanase activity; enzyme; thermostable; xylanase; pulp bleaching;
KW liquid clarification; coffee extraction; plant oil extraction;
KW starch extraction; food thickener; animal food additive; mutant; mutein.
XX OS Bacillus subtilis.
XX PN WO200238746-A2.
XX PD 16-MAY-2002.
XX PF 09-NOV-2001; 2001WO-US048018.
XX PR 10-NOV-2000; 2000US-00710050.
XX PA (XENC-) XENCOR INC.
XX PT Bentzien J, Dahiyat B;
XX PI WPI; 2002-608200/65.
XX DR Novel xylanase activity protein, useful in bleaching process of pulp and
PT in food and animal feed industry, has enhanced thermostability and
PT alkalophilicity.
XX PS Disclosure; Fig 16A; 121pp; English.
XX
CC The present invention relates to a non-naturally occurring xylanase
CC activity (XA) protein comprising an amino acid sequence less than 97%
CC identical to a naturally occurring Bacillus circulans xylanase, where the
CC protein has been modified to exhibit enhanced thermophilicity,
CC alkalophilicity, or thermostability relative to naturally occurring B.

XX WPI; 2000-679800/66.
XX Non naturally occurring XA protein with enhanced thermophilicity,
PT alkalophilicity or thermostability relative to the naturally occurring
PT Bacillus circulans xylanase is used in an agent for bleaching pulp.
XX
XX
PS Disclosure; Fig 16A; 114pp; English.
XX
CC The present sequence is given in a specification relating to non
CC naturally occurring xylanase activity (XA) proteins. The XA proteins
CC comprise an amino acid sequence less than 97% identical to a naturally
CC occurring Bacillus circulans xylanase. They are modified to exhibit
CC enhanced thermophilicity, alkalophilicity or thermostability relative to
CC the naturally occurring B. circulans xylanase. They may be used as the
CC active compound in a bleaching agent which is used for bleaching pulp
XX
SQ Sequence 213 AA;
Query Match 99.7%; Score 1168; DB 3; Length 213;
Best Local Similarity 99.5%; Pred. No. 3.3e-91;
Matches 212; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MFKEKQFLVGLSAALMSISLFSATASASTDYQNQNTDGGGIYNAVNGSGGYSVNVNSN 60
Db 1 MFKEKQFLVGLSAALMSISLFSATASASTDYQNQNTDGGGIYNAVNGSGGYSVNVNSN 60
Qy 61 TGNFVVGKGTGSPFRTINYNAGVWAPNGNGYLTLYGWTRSPLEIYYVVDVDSWGTYRPTG 120
Db 61 TGNFVVGKGTGSPFRTINYNAGVWAPNGNGYLTLYGWTRSPLEIYYVVDVDSWGTYRPTG 120
Qy 121 TYKGTVKS DGGTYDIYITTRYNAPSIDGDRITFTQYWSVRQSKRPTGSNATITFTNHVNA 180
Db 121 TYKGTVKS DGGTYDIYITTRYNAPSIDGDRITFTQYWSVRQSKRPTGSNATITFTNHVNA 180
Qy 181 WKSHGMNLGSNWAYQVNWATEGYQSSGSSNVTW 213
Db 181 WKSHGMNLGSNWAYQVNWATEGYQSSGSSNVTW 213
RESULT 6
AAB48518
ID AAB48518 standard; protein; 213 AA.
XX AC AAB48518;
XX DT 05-MAR-2001 (first entry)
XX DE Bacillus circulans endo-1,4-beta xylanase precursor.
XX KW Bacillus circulans; xylanase; xylanase activity; XA; bleaching agent.
XX OS Bacillus circulans.
XX PN WO2000068396-A2.
XX PD 16-NOV-2000.
XX PF 12-MAY-2000; 2000WO-US013172.
XX PR 12-MAY-1999; 99US-0133714P.
XX PA (XENC-) XENCOR INC.
XX PI Bentzien JM;
XX PS WPI; 2000-679800/66.
XX
CC Non naturally occurring XA protein with enhanced thermophilicity,
PT alkalophilicity or thermostability relative to the naturally occurring
PT Bacillus circulans xylanase is used in an agent for bleaching pulp.
XX
XX
PS Disclosure; Fig 1A; 114pp; English.

CC circulans xylanase, and has at least 5 amino acid substitutions. A
CC bleaching agent comprising a modified xylanase is useful for bleaching
CC pulp, in the bioconversion of lignocellulosic materials to fuels, for
CC clarifying juice and wine, extracting coffee, plant oils and starch,
CC producing food thickeners, altering texture in bakery products, e.g.
CC improving the quality of dough, helping bread to rise and processing of
CC wheat and corn for starch production, use as animal food additives to aid
CC in the digestibility of feedstuffs and in the washing of super precision
CC devices and semiconductors. The present sequence is a xylanase protein
CC described in the exemplification of the invention
XX
SQ Sequence 213 AA;

Query Match 99.7%; Score 1168; DB 5; Length 213;
Best Local Similarity 99.5%; Pred. No. 3.3e-91;
Matches 212; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MFKFKNFVLGLSALMSISLFSATASASTDYQWNTDGGIYNVANGSGNYVNSN 60
Db 1 MFKFKNFVLGLSALMSISLFSATASASTDYQWNTDGGIYNVANGSGNYVNSN 60
Qy 61 TGNFVVGKWTGSPFRTINYNAGVWAPNGNGYLYLWGTRSPLEIYYVVDVSWGTYRPTG 120
Db 61 TGNFVVGKWTGSPFRTINYNAGVWAPNGNGYLYLWGTRSPLEIYYVVDVSWGTYRPTG 120
Qy 121 TYKGTVKSDGGTYDIYTTTRYNAPSIDGDRFTTQYWSVRQSKRPTGNSNHNVA 180
Db 121 TYKGTVKSDGGTYDIYTTTRYNAPSIDGDRFTTQYWSVRQSKRPTGNSNHNVA 180
Qy 181 WKSHGMNLGNSWAYQVMATEGYQSSGSSNVTW 213
Db 181 WKSHGMNLGNSWAYQVMATEGYQSSGSSNVTW 213

RESULT 8
AAO18624
ID AAO18624 standard; protein; 213 AA.
AC AAO18624;
XX
XX
DT 24-OCT-2002 (first entry)
XX
DE Endo-1,4-beta xylanase precursor protein.
XX
XX Xylanase activity; enzyme; thermostable; xylanase; pulp bleaching;
KW liquid clarification; coffee extraction; plant oil extraction;
KW starch extraction; food thickener; animal food additive; mutant; mutein.
XX
OS Unidentified.
XX
XX WO200238746-A2.
XX
XX 16-MAY-2002.
XX
XX 09-NOV-2001; 2001WO-US048018.
XX
XX 10-NOV-2000; 2000US-00710050.
XX
XX (XENC-) XENCOR INC.
XX
XX Bentzien J, Dahiyat B;
XX
XX WPI; 2002-608200/65.
XX
XX Novel xylanase activity protein, useful in bleaching process of pulp and
PT in food and animal feed industry, has enhanced thermostability and
PT alkalophilicity.
XX
XX Disclosure; Fig 1A; 121pp; English.
XX
XX The present invention relates to a non-naturally occurring xylanase
XC activity (XA) protein comprising an amino acid sequence less than 97%
CC identical to a naturally occurring Bacillus circulans xylanase, where the

CC protein has been modified to exhibit enhanced thermophilicity,
CC alkalophilicity, or thermostability relative to naturally occurring B.
CC circulans xylanase, and has at least 5 amino acid substitutions. A
CC bleaching agent comprising a modified xylanase is useful for bleaching
CC pulp, in the bioconversion of lignocellulosic materials to fuels, for
CC clarifying juice and wine, extracting coffee, plant oils and starch,
CC producing food thickeners, altering texture in bakery products, e.g.
CC improving the quality of dough, helping bread to rise and processing of
CC wheat and corn for starch production, use as animal food additives to aid
CC in the digestibility of feedstuffs and in the washing of super precision
CC devices and semiconductors. The present sequence is a xylanase protein
CC described in the exemplification of the invention
XX
SQ Sequence 213 AA;

Query Match 99.7%; Score 1168; DB 5; Length 213;
Best Local Similarity 99.5%; Pred. No. 3.3e-91;
Matches 212; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MFKFKNFVLGLSALMSISLFSATASASTDYQWNTDGGIYNVANGSGNYVNSN 60
Db 1 MFKFKNFVLGLSALMSISLFSATASASTDYQWNTDGGIYNVANGSGNYVNSN 60
Qy 61 TGNFVVGKWTGSPFRTINYNAGVWAPNGNGYLYLWGTRSPLEIYYVVDVSWGTYRPTG 120
Db 61 TGNFVVGKWTGSPFRTINYNAGVWAPNGNGYLYLWGTRSPLEIYYVVDVSWGTYRPTG 120
Qy 121 TYKGTVKSDGGTYDIYTTTRYNAPSIDGDRFTTQYWSVRQSKRPTGNSNHNVA 180
Db 121 TYKGTVKSDGGTYDIYTTTRYNAPSIDGDRFTTQYWSVRQSKRPTGNSNHNVA 180
Qy 181 WKSHGMNLGNSWAYQVMATEGYQSSGSSNVTW 213
Db 181 WKSHGMNLGNSWAYQVMATEGYQSSGSSNVTW 213

RESULT 9
ADJ35008
ID ADJ35008 standard; protein; 213 AA.
XX
XX AC ADJ35008;
XX
XX
DT 22-APR-2004 (first entry)
XX
XX Xylanase from an environmental sample seq id 224.
DE
DE antibacterial; fungicide; thermostable xylanase activity;
KW dough conditioning; beverage production; nutritional supplement;
KW animal feed; lignin reduction; wood product; xylan; bacterial infection;
KW fungal infection; coccidioides.
XX
XX Unidentified.
XX
XX WO2003106654-A2.
XX
XX 24-DEC-2003.
XX
XX 16-JUN-2003; 2003WO-US019153.
XX
XX 14-JUN-2002; 2002US-0389299P.
XX
XX (DIVE-) DIVERSA CORP.
XX
XX Steer B, Callen W, Healey S, Hazlewood G, Wu D, Blum D;
PI Esteghlalian A;
XX
XX WPI; 2004-099016/10.
DR N-PSDB; ADJ35007.
XX
XX Novel xylanase recombinant polypeptide useful for improving textile
PT texture, treating paper, eliminating microorganisms.
XX
XX Claim 60; SEQ ID NO 224; 570pp; English.
PS

XX The invention describes an isolated or recombinant polypeptide (I),
CC having 50% or more identity to 190 300-1200 residue amino acid sequences
CC (S1), given in the specification, over a region of 100 or more residues
CC and the polypeptide as thermostable xylanase activity. (I) is useful for:
CC dough conditioning; beverage production; as a nutritional supplement in
CC animal feed; reducing lignin in a wood or a wood product; and for
CC eliminating and protecting animals from a microorganism comprising xylan.
CC The polynucleotide (II) encoding (I) is useful for amplifying nucleic
CC acid encoding a polypeptide having a xylanase activity which involves
CC amplification of a template nucleic acid with a primer pair capable of
CC amplifying (II) or its subsequence. (I) is useful for treating and
CC preventing bacterial infection and fungal infection e.g. coccidiosis.
CC This is the amino acid sequence of a xylanase protein isolated from an
CC environmental sample.

XX SQ Sequence 213 AA;

Query Match 99.7%; Score 1168; DB 8; Length 213;
Best Local Similarity 99.5%; Pred. No. 3.3e-91;
Matches 212; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFEPKKNFLVGLSAAALMSISLFSATASASTDYQNNWTDGGGIYNAVNGSGGNYSVNWSN 60
Db 1 MFEPKKNFLVGLSAAALMSISLFSATASASTDYQNNWTDGGGIYNAVNGSGGNYSVNWSN 60
Qy 61 TGNFVVGKWTGSPFRTINYNAGVWAPNGNGYLYLGWTRSPLEIYYVVDWSGTYRPTG 120
Db 61 TGNFVVGKWTGSPFRTINYNAGVWAPNGNGYLYLGWTRSPLEIYYVVDWSGTYRPTG 120
Qy 121 TYKGTVKSDGGTYDIYTTTTRYNAPSIDGDRITFTQYWSVRQSKRPTGSNATITFSNHVNA 180
Db 121 TYKGTVKSDGGTYDIYTTTTRYNAPSIDGDRITFTQYWSVRQSKRPTGSNATITFSNHVNA 180
Qy 181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTVW 213
Db 181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTVW 213

RESULT 10
ADI66728
ID ADI66728 standard; protein; 213 AA.

XX AC ADI66728;

XX DT 22-APR-2004 (first entry)

XX DE B. circulans endo-1,4-beta xylanase.

XX Endo-1,4-beta xylanase; XA; EC 3.2.1.8; enzyme; bleaching;
KW bleaching pulp; paper industry; food; animal feed; thermostability;
KW alkalophilic; hot alkali treatment.

XX OS Bacillus circulans.

XX FH Key Location/Qualifiers
FT Peptide 1..28
FT Protein /note= "Signal peptide"
FT Protein 29..213
FT Protein /note= "Mature Xylanase"

XX US6682923-B1.

XX PD 27-JAN-2004.

XX PF 12-MAY-2000; 2000US-00570856.

XX PR 12-MAY-1999; 99US-0133714P.

XX PR 07-JUN-1999; 99US-0138156P.

XX PA (XENC-) XENCOR.

XX PI Bentzien J, Dahiyat BI;

XX DR

WPI; 2004-118575/12.
N-PSDB; ADI66729.

XX New mutant xylanase (XA) protein comprising at least four amino acid
PT substitutions as compared to Bacillus circulans xylanase, useful for
PT bleaching (paper) pulp, and in the food and animal feed industries.

XX Claim 2; SEQ ID NO 1; 84pp; English.

XX The invention relates to a mutant xylanase activity (XA, endo-1,4-beta
CC xylanase from Bacillus circulans) protein appearing as ADI66730. Also
CC included is a bleaching agent comprising the XA protein. The non-
CC naturally occurring XA protein comprises at least four amino acid
CC substitutions as compared to Bacillus circulans xylanase ADI66728. The
CC amino acid substitutions are made at positions 26, 28, 30, 53, 58, 64,
CC 79, 105, 142, 144, 171, 176, 180 or 182, especially at positions 28, 30,
CC 58, or 144. The non-naturally occurring xylanase activity (XA) protein is
CC useful for bleaching pulp in the paper and related industries, but is
CC also useful in the food and animal feed industries. The new protein is
CC active at higher pH and temperature ranges than naturally occurring
CC xylanases, simplifying incorporation of the xylanase treatment step into
CC pulp processing, especially where the enzyme is added after hot alkali
CC treatment. The present sequence represents the wild-type xylanase.

XX SQ Sequence 213 AA;

Query Match 99.7%; Score 1168; DB 8; Length 213;
Best Local Similarity 99.5%; Pred. No. 3.3e-91;
Matches 212; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFEPKKNFLVGLSAAALMSISLFSATASASTDYQNNWTDGGGIYNAVNGSGGNYSVNWSN 60
Db 1 MFEPKKNFLVGLSAAALMSISLFSATASASTDYQNNWTDGGGIYNAVNGSGGNYSVNWSN 60
Qy 61 TGNFVVGKWTGSPFRTINYNAGVWAPNGNGYLYLGWTRSPLEIYYVVDWSGTYRPTG 120
Db 61 TGNFVVGKWTGSPFRTINYNAGVWAPNGNGYLYLGWTRSPLEIYYVVDWSGTYRPTG 120
Qy 121 TYKGTVKSDGGTYDIYTTTTRYNAPSIDGDRITFTQYWSVRQSKRPTGSNATITFSNHVNA 180
Db 121 TYKGTVKSDGGTYDIYTTTTRYNAPSIDGDRITFTQYWSVRQSKRPTGSNATITFSNHVNA 180
Qy 181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTVW 213
Db 181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTVW 213

RESULT 11

ADI66740

ID ADI66740 standard; protein; 213 AA.

XX AC ADI66740;

XX DT 22-APR-2004 (first entry)

XX DE B. subtilis xylanase.

XX Xylanase; XA; EC 3.2.1.8; enzyme; bleaching; bleaching pulp;
KW paper industry; food; animal feed; thermostability; alkalophilic;
KW hot alkali treatment.

XX OS Bacillus subtilis.

XX US6682923-B1.

XX PD 27-JAN-2004.

XX PF 12-MAY-2000; 2000US-00570856.

XX PR 12-MAY-1999; 99US-0133714P.

XX PR 07-JUN-1999; 99US-0138156P.

(XENC-) XENCOR.
Bentzien J, Dahiyat BI;
WPI; 2004-118575/12.
New mutant xylanase (XA) protein comprising at least four amino acid substitutions as compared to Bacillus circulans xylanase, useful for bleaching (paper) pulp, and in the food and animal feed industries.
Disclosure; SEQ ID NO 13; 84pp; English.
The invention relates to a mutant xylanase activity (XA, endo-1,4-beta xylanase from Bacillus circulans) protein appearing as ADI66730. Also included is a bleaching agent comprising the XA protein. The non-naturally occurring XA protein comprises at least four amino acid substitutions as compared to Bacillus circulans xylanase ADI66728. The amino acid substitutions are made at positions 26, 28, 30, 53, 58, 64, 79, 105, 142, 144, 171, 176, 180 or 182, especially at positions 28, 30, 58, or 144. The non-naturally occurring xylanase activity (XA) protein is useful for bleaching pulp in the paper and related industries, but is also useful in the food and animal feed industries. The new protein is active at higher pH and temperature ranges than naturally occurring xylanases, simplifying incorporation of the xylanase treatment step into pulp processing, especially where the enzyme is added after hot alkali treatment. The present sequence is a xylanase from another species included for comparison.
XX Sequence 213 AA;
SQ

Query Match 99.7%; Score 1168; DB 8; Length 213;
Best Local Similarity 99.5%; Pred. No. 3.3e-91;
Matches 212; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MFKKKFLVGLSALMSISLFSATASAASTDYQWNTDGGIYNAVNGSGSYVNSN 60
Db 1 MFKKKFLVGLSALMSISLFSATASAASTDYQWNTDGGIYNAVNGSGSYVNSN 60
Qy 61 TGNFVVGKWTGSPFRITINYNAGWAPNGNGYLTLYGWTSPLEIYYVVDVDSWGTYRPTG 120
Db 61 TGNFVVGKWTGSPFRITINYNAGWAPNGNGYLTLYGWTSPLEIYYVVDVDSWGTYRPTG 120
Qy 121 TYKGTVSDGGTYDIYTTTRYNAPSIDGDRFTTQYWSVRSKRPSTGNSNATITFSNHVA 180
Db 121 TYKGTVSDGGTYDIYTTTRYNAPSIDGDRFTTQYWSVRSKRPSTGNSNATITFSNHVA 180
Qy 181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTW 213
Db 181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTW 213

RESULT 12
RAY93755
ID AAY93755 standard; protein; 213 AA.
XX
AC AAY93755;
XX
DT 03-OCT-2000 (first entry)
XX
DE A bacterial endo-beta-1,4-xylanase mutant XM3.
XX
KW Endo-beta-1,4-xylanase inhibitor; wheat flour; xylanase; bakery product;
XX dough; dough preparation.
XX
OS Synthetic.
OS Bacillus subtilis.
XX WO200039289-A2.
XX
PD 06-JUL-2000.
XX
PF 17-DEC-1999; 99WO-IB002071.
XX

23-DEC-1998; 98GB-00028599.
06-APR-1999; 99GB-00007805.
15-APR-1999; 99GB-00008645.
(DANI-) DANISCO AS.
Sibbesen O, Sorensen JF;
WPI; 2000-465744/40.
N-ESDB; AAA47157.
Mutant xylanase protein identified using xylanase inhibitor useful for preparing non-sticky dough for bakery products.
Claim 1; Page 111; 112pp; English.
The present sequence represents a mutant endo-beta-1,4-xylanase. The specification also describes an endo-beta-1,4-xylanase inhibitor, which is obtained from wheat flour. The specification also describes a mutant xylanase protein. The xylanase is useful for preparing a foodstuff, preferably a bakery product or a substance (e.g. a dough) for making the bakery product. Wild type xylanase or mutant xylanase is useful for preparing a dough that is less sticky than a dough comprising a fungal xylanase. The xylanase inhibitor is useful for screening high degree resistance xylanases for dough preparation. The xylanase is also useful for preparing a non-sticky dough. A combination of xylanase and the inhibitor is useful for calibrating and/or determining the quantity of inhibitor in a wheat flour sample
XX Sequence 213 AA;
SQ

Query Match 99.1%; Score 1161; DB 3; Length 213;
Best Local Similarity 99.1%; Pred. No. 1.3e-90;
Matches 211; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 MFKKKFLVGLSALMSISLFSATASAASTDYQWNTDGGIYNAVNGSGSYVNSN 60
Db 1 MFKKKFLVGLSALMSISLFSATASAASTDYQWNTDGGIYNAVNGSGSYVNSN 60
Qy 61 TGNFVVGKWTGSPFRITINYNAGWAPNGNGYLTLYGWTSPLEIYYVVDVDSWGTYRPTG 120
Db 61 TGNFVVGKWTGSPFRITINYNAGWAPNGNGYLTLYGWTSPLEIYYVVDVDSWGTYRPTG 120
Qy 121 TYKGTVSDGGTYDIYTTTRYNAPSIDGDRFTTQYWSVRSKRPSTGNSNATITFSNHVA 180
Db 121 TYKGTVSDGGTYDIYTTTRYNAPSIDGDRFTTQYWSVRSKRPSTGNSNATITFSNHVA 180
Qy 181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTW 213
Db 181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTW 213

RESULT 13
RAY93753
ID AAY93753 standard; protein; 213 AA.
XX
AC AAY93753;
XX
DT 03-OCT-2000 (first entry)
XX
DE A bacterial endo-beta-1,4-xylanase mutant XM1.
XX
KW Endo-beta-1,4-xylanase inhibitor; wheat flour; xylanase; bakery product;
XX dough; dough preparation.
XX
OS Synthetic.
OS Bacillus subtilis.
XX
FH Key Location/Qualifiers
FT Misc-difference 43 /note= "wild type Ile changed to Thr"
FT Misc-difference 197 /note= "wild type Met changed to Leu"
FT

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FT Misc-difference 203
FT /note= "wild type Gln changed to Lys"
XX
XX
XX WO200039289-A2.
XX
XX PD 06-JUL-2000.
XX
XX PF 17-DEC-1999; 99WO-IB002071.
XX
XX PR 23-DEC-1998; 98GB-00028599.
XX PR 06-APR-1999; 99GB-00007805.
XX PR 15-APR-1999; 99GB-00008645.
XX
XX PA (DANI-) DANISCO AS.
XX
XX PI Sibbesen O, Sorensen JF;
XX
XX DR WPI; 2000-465744/40.
XX DR N-PSDB; AAA47155.
XX
XX PT Mutant xylanase protein identified using xylanase inhibitor useful for
XX preparing non-sticky dough for bakery products.
XX
XX PS Claim 1; Page 109; 112pp; English.
XX
XX CC The present sequence represents a mutant endo-beta-1,4-xylanase. The
XX specification also describes an endo-beta-1,4-xylanase inhibitor, which
XX is obtained from wheat flour. The specification also describes a mutant
XX xylanase protein. The xylanase is useful for preparing a foodstuff,
XX preferably a bakery product or a substance (e.g. a dough) for making the
XX bakery product. Wild type xylanase or mutant xylanase is useful for
XX preparing a dough that is less sticky than a dough comprising a fungal
XX xylanase. The xylanase inhibitor is useful for screening high degree
XX resistance xylanases for dough preparation. The xylanase is also useful
XX for preparing a non-sticky dough. A combination of xylanase and the
XX inhibitor is useful for calibrating and/or determining the quantity of
XX inhibitor in a wheat flour sample
XX
XX SQ Sequence 213 AA;
XX
XX Query Match 98.5%; Score 1154; DB 3; Length 213;
XX Best Local Similarity 98.1%; Pred. No. 5.1e-90;
XX Matches 209; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
XX
XX Qy 1 MFKFKQFLVGLSAALMSISLFSATASAASTDYQWNTDGGGIYNAVNGSGGNTSVNWSN 60
XX Db 1 MFKFKQFLVGLSAALMSISLFSATASAASTDYQWNTDGGGIYNAVNGSGGNTSVNWSN 60
XX
XX Qy 61 TGNFVVGKGTGSPFRTINYNAGVWAPNGNGYLTLYGWTRSPLEIYYVVDWSGTYRPTG 120
XX Db 61 TGNFVVGKGTGSPFRTINYNAGVWAPNGNGYLTLYGWTRSPLEIYYVVDWSGTYRPTG 120
XX
XX Qy 121 TYKGTVKSDDGTYDIYITTRYNAPSIDGDRITFTQYWSVRQSKRPTGSNATITFSNHVNA 180
XX Db 121 TYKGTVKSDDGTYDIYITTRYNAPSIDGDRITFTQYWSVRQSKRPTGSNATITFSNHVNA 180
XX
XX Qy 181 WKSHGMNLGSNWAYQVWATEGYQSSGSSNTVTW 213
XX Db 181 WKSHGMNLGSNWAYQVWATEGYQSSGSSNTVTW 213
XX
XX RESULT 14
XX ID AAY93754 standard; protein; 213 AA.
XX
XX AC AAY93754;
XX
XX XX 03-OCT-2000 (first entry)
XX
XX DE A bacterial endo-beta-1,4-xylanase mutant XM2.
XX
XX KW Endo-beta-1,4-xylanase inhibitor; wheat flour; xylanase; bakery product;
XX dough; dough preparation.
```

```
XX
XX Synthetic.
XX Bacillus subtilis.
XX
XX FN WO200039289-A2.
XX
XX PD 06-JUL-2000.
XX
XX PF 17-DEC-1999; 99WO-IB002071.
XX
XX PR 23-DEC-1998; 98GB-00028599.
XX PR 06-APR-1999; 99GB-00007805.
XX PR 15-APR-1999; 99GB-00008645.
XX
XX PA (DANI-) DANISCO AS.
XX
XX PI Sibbesen O, Sorensen JF;
XX
XX DR WPI; 2000-465744/40.
XX DR N-PSDB; AAA47155.
XX
XX PT Mutant xylanase protein identified using xylanase inhibitor useful for
XX preparing non-sticky dough for bakery products.
XX
XX PS Claim 1; Page 110; 112pp; English.
XX
XX CC The present sequence represents a mutant endo-beta-1,4-xylanase. The
XX specification also describes an endo-beta-1,4-xylanase inhibitor, which
XX is obtained from wheat flour. The specification also describes a mutant
XX xylanase protein. The xylanase is useful for preparing a foodstuff,
XX preferably a bakery product or a substance (e.g. a dough) for making the
XX bakery product. Wild type xylanase or mutant xylanase is useful for
XX preparing a dough that is less sticky than a dough comprising a fungal
XX xylanase. The xylanase inhibitor is useful for screening high degree
XX resistance xylanases for dough preparation. The xylanase is also useful
XX for preparing a non-sticky dough. A combination of xylanase and the
XX inhibitor is useful for calibrating and/or determining the quantity of
XX inhibitor in a wheat flour sample
XX
XX SQ Sequence 213 AA;
XX
XX Query Match 98.1%; Score 1149; DB 3; Length 213;
XX Best Local Similarity 97.7%; Pred. No. 1.3e-89;
XX Matches 208; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
XX
XX Qy 1 MFKFKQFLVGLSAALMSISLFSATASAASTDYQWNTDGGGIYNAVNGSGGNTSVNWSN 60
XX Db 1 MFKFKQFLVGLSAALMSISLFSATASAASTDYQWNTDGGGIYNAVNGSGGNTSVNWSN 60
XX
XX Qy 61 TGNFVVGKGTGSPFRTINYNAGVWAPNGNGYLTLYGWTRSPLEIYYVVDWSGTYRPTG 120
XX Db 61 TGNFVVGKGTGSPFRTINYNAGVWAPNGNGYLTLYGWTRSPLEIYYVVDWSGTYRPTG 120
XX
XX Qy 121 TYKGTVKSDDGTYDIYITTRYNAPSIDGDRITFTQYWSVRQSKRPTGSNATITFSNHVNA 180
XX Db 121 TYKGTVKSDDGTYDIYITTRYNAPSIDGDRITFTQYWSVRQSKRPTGSNATITFSNHVNA 180
XX
XX Qy 181 WKSHGMNLGSNWAYQVWATEGYQSSGSSNTVTW 213
XX Db 181 WKSHGMNLGSNWAYQVWATEGYQSSGSSNTVTW 213
XX
XX RESULT 15
XX ID AAR47200 standard; protein; 213 AA.
XX
XX AC AAR47200;
XX
XX XX 25-MAR-2003 (revised)
XX DT 10-AUG-1994 (first entry)
XX
XX DE Modified xylanase of Bacillus subtilis.
XX
```

KW Xylanase; Bacillus subtilis; baking; bread; yeast; food; foodstuffs;
KW bread; pastry.

XX Bacillus subtilis.

XX Key Location/Qualifiers
XX PH Peptide 1..28
FT /label= Signal peptide.

FT Misc-difference 7 /note= "Wild type amino acid substituted for Lys."
FT Misc-difference 13 /note= "Wild type amino acid substituted for Thr."
FT Misc-difference 16 /note= "Wild type amino acid substituted for Phe."
FT Misc-difference 21 /note= "Wild type amino acid substituted for Met."
FT Peptide 29..185
FT /label= Mature protein.
FT Misc-difference 30 /note= "Wild type amino acid substituted for Gly."
FT Misc-difference 43 /note= "Wild type amino acid substituted for Thr."
FT Misc-difference 150 /note= "Wild type amino acid substituted for Asn."
FT Misc-difference 171 /note= "Wild type amino acid substituted for Ala."
FT Misc-difference 197 /note= "Wild type amino acid substituted for Leu."
FT Misc-difference 203 /note= "Wild type amino acid substituted for Lys."

XX DE4226528-A1.

XX 17-FEB-1994.

XX 11-AUG-1992; 92DE-04226528.

XX 11-AUG-1992; 92DE-04226528.

XX (ROHG) ROEHM GMBH.

XX Gottschalk M, Sproessler B, Schuster E;

XX WPI; 1994-058089/08.

XX N-PSDB; AAQ56052.

XX New xylanase obtd. from Bacillus subtilis - useful in baking agents for
XX increased vol. of baking prods.

XX Claim 4; Page 10; lipp; German.

XX The modified xylanase is used as a baking agent, preferably for yeast
XX pastry and white bread. (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 213 AA;

Query Match 96.5%; Score 1130; DB 2; Length 213;
Best Local Similarity 95.3%; Pred. No. 5, 6e-88;
Matches 203; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 1 MFKFKNLFVLGSLAALMSISLFSATASAASTDYQWQNTDGGGVNAVNGSGNGYSVNWNSN 60

Db 1 MFKPKKFLVGLTAAFMSISMFSAATAAGTDYQWQNTDGGGVNAVNGSGNGYSVNWNSN 60

Qy 61 TGNFVVGKWTGSPFRINYNAGVWAPNGCYLTYGWTSPLEIYYVVDWSWGTYRPTG 120

Db 61 TGNFVVGKWTGSPFRINYNAGVWAPNGCYLTYGWTSPLEIYYVVDWSWGTYRPTG 120

Qy 121 TYKGVTKSGGGTYDIYTTTRYNAPSIDGDRITFTQYWSVROSKRPTGSAATITFSNHVNA 180

Db 121 TYKGVTKSGGGTYDIYTTTRYNAPSIDGDRITFTQYWSVROSKRPTGSAATITFSNHVNA 180

Qy 181 WKSHGMNLGSNWAYQVATEGYQSSGSSNVTVW 213

Db 181 WKSHGMNLGSNWAYQVATEGYKSSGSSNVTVW 213

Search completed: February 3, 2006, 09:08:08
Job time : 201 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 3, 2006, 09:04:53 ; Search time 246 Seconds
(without alignments)
610.884 Million cell updates/sec

Title: US-10-626-724-5

Perfect score: 1171

Sequence: 1 MFKPKNPLVGLSAAALMSIS.....YQVMATEQYQSSGSSNTVTW 213

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1171	100.0	213	1 Xyna_BACSU	P18429 bacillus su
2	1168	99.7	213	1 Xyna_BACCI	P09850 bacillus su
3	1166	99.6	213	2 Q59254 BACSU	Q59254 bacillus su
4	1165	99.5	213	2 Q59256 9BACI	Q59256 bacillus sp
5	1150	98.2	213	2 Q8RMN9 BACSU	Q8RMN9 bacillus su
6	1144	97.7	213	2 Q8RMN8 BACCI	Q8RMN8 bacillus ci
7	1127	96.2	213	2 Q92B36 BACSP	Q92B36 bacillus sp
8	1104	94.3	213	2 Q84F19 9BACI	Q84F19 bacillus sp
9	1096	93.6	213	2 Q8VVC3 9BACI	Q8VVC3 bacillus sp
10	945.5	80.7	212	2 Q9F9B9 9BACL	Q9F9B9 paenibacill
11	935.5	79.9	214	2 Q6TLP3 9BACT	Q6TLP3 uncultured
12	930	79.4	210	1 Xyna_BACST	P45705 bacillus st
13	929	79.3	211	2 Q43993 AERPU	Q43993 aeromonas p
14	864.5	73.8	210	2 Q71S35 BACFI	Q71S35 bacillus fi
15	864.5	73.8	210	2 Q9KEF3 BACHD	Q9KEF3 bacillus ha
16	863.5	73.7	210	2 Q6U894 BACFI	Q6U894 bacillus fi
17	663.5	56.7	335	2 Q9RQB8 9MICO	Q9RQB8 xylanimicro
18	659	56.3	338	2 Q56265 THEFU	Q56265 thermomonos
19	659	56.3	338	2 Q5RZ98 THEFU	Q5RZ98 thermomonos
20	651.5	55.6	241	2 Q9RMH9 9BACI	Q9RMH9 streptomyc
21	646	55.2	329	2 Q9RMH9 STRVD	Q9RMH9 streptomyc
22	645.5	55.1	335	2 Q9RMH4 STRFM	Q9RMH4 streptomyc
23	639.5	54.6	335	2 Q76BV2 STRTL	Q76BV2 streptomyc
24	637	54.4	240	1 XINC STRLI	P26220 streptomyc
25	630	53.8	344	2 Q8GMV7 9ACTO	Q8GMV7 nonomuraea
26	626	53.5	191	2 Q9EM89 STROI	Q9EM89 streptomyc
27	622	53.1	228	2 Q59962 9ACTO	Q59962 streptomyc
28	621.5	53.1	228	2 Q4WG11 ASPFU	Q4WG11 aspergillus
29	621	53.0	240	2 Q56013 9ACTO	Q56013 streptomyc
30	610.5	52.1	417	2 Q693B5 9ALTE	Q693B5 microbulbif
31	609.5	52.0	644	1 XYND_CELFI	P54865 cellulomona

RESULT 1				
XYNA	BACSU	STANDARD;	PRT;	213 AA.
ID	XYNA_BACSU			
AC	P18429;			
DT	01-NOV-1990 (Rel. 16, Created)			
DT	01-NOV-1990 (Rel. 16, Last sequence update)			
DT	10-MAY-2005 (Rel. 47, Last annotation update)			
DE	Endo-1,4-beta-xylanase A precursor (EC 3.2.1.8) (Xylanase A) (1,4-			
DE	beta-D-xylan xylanohydrolase A).			
GN	Name=xyNA; OrderedLocusNames=BSU18840;			
OS	Bacillus subtilis.			
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.			
OX	NCBI_TaxID=1423;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RA	Paice M.G., Bourbonnais R., Desrochers M., Jurasek L., Yaguchi M.;			
RT	"A xylanase gene from Bacillus subtilis: nucleotide sequence and			
RT	comparison with B. pumilus gene.;"			
RL	Arch. Microbiol. 144:201-206(1986).			
RN	[2]			
RP	NUCLEOTIDE SEQUENCE.			
RA	Lapidus A., Galleron N., Sorokin A., Ehrlich S.D.;			
RT	"Sequence analysis of the Bacillus subtilis chromosome region between			
RT	the terC and ohaB loci cloned in a yeast artificial chromosome.;"			
RL	Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.			
RN	[3]			
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].			
RC	STRAIN=168;			
RX	MEDLINE=98044033; PubMed=9384377; DOI=10.1038/36786;			
RA	Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,			
RA	Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,			
RA	Borries R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,			
RA	Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,			
RA	Choi S.-K., Codani J.-J., Connerton I.F., Cummings N.J., Daniel R.A.,			
RA	Denizot F., Devine K.M., Duesterhoeft A., Ehrlich S.D., Emmerson P.T.,			
RA	Entian K.-D., Errington J., Fabret C., Ferrari E., Foulger D.,			
RA	Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,			
RA	Ghim S.-Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,			
RA	Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,			
RA	Hilbert H., Holsappel S., Hosono S., Hullo M.-F., Itaya M.,			
RA	Jones L.-M., Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M.,			
RA	Klein C., Kobayashi Y., Koetter P., Koningsstein G., Krogh S.,			
RA	Kumano M., Kurita K., Lapidus A., Lardinois S., Lauber J.,			
RA	Lazarevic V., Lee S.-M., Levine A., Liu H., Masuda S., Maue C.,			
RA	Medigue C., Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S.,			
RA	Noback M., Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B.,			
RA	Park S.-H., Parro V., Pohl T.M., Portetelle D., Porwollik S.,			
RA	Prescott A.M., Presecan E., Pujic P., Purnelle B., Rapoport G.,			
RA	Rey M., Reynolds S., Rieger M., Rivolta C., Rocha E., Roche B.,			
RA	Rose M., Sadaie Y., Sato T., Scanlan E., Schleich S., Schroeter R.,			
RA	Scoffone F., Sekiguchi J., Sekowska A., Seror S.J., Serror P.,			
RA	Shin B.-S., Soldo B., Sorokin A., Tacconi E., Takagi T., Takahashi H.,			
RA	Takemaru K., Takeuchi M., Tamakoshi A., Tanaka T., Terpsira P.,			
RA	Tognoni A., Tosato V., Uchiyama S., Vandenbol M., Vannier F.,			

Q8VUT4 pseudomonas
P53332 emericella
Q5B767 aspergillus
P26515 streptomyc
Q9KN6 streptomyc
Q7ADQ1 neurospora
Q81V5 chaetomium
Q8CG22 aspergillus
Q6GA21 aspergillus
Q5AGR5 aspergillus
P55330 aspergillus
Q9HFA4 aspergillus
P53333 emericella
P48824 aspergillus

RA Vassarotti A., Viari A., Wambutt R., Wedler E., Wedler H.,
RA Weitzenecker T., Winters P., Wipat A., Yamamoto H., Yamane K.,
RA Yasumoto K., Yata K., Yoshida K., Yoshikawa H.-F., Zimstein E.,
RA Yoshikawa H., Danchin A.;
RT "The complete genome sequence of the Gram-positive bacterium *Bacillus*
RT subtilisRL Nature 390:249-256(1997).
RN [4];
RN MUTAGENESIS.
RP W&Karchuk W., Methot N., Lanthier P., Sung W., Seligy V., Yaguchi M.,
RA To R., Campbell R., Rose D.;
RA (In) Visser J., Beldman G., Kusters-van Sommeren M.A., Voragen A.G.J.
RL (eds.);
RL Xylans and xylanases, pp.439-442, Elsevier, Amsterdam (1992).
RN [5];
RN ACTIVE SITE GLU-106.
RX MEDLINE=94271752; PubMed=7911679;
RA Miao S., Ziser L., Abersold R., Withers S.G.;
RT "Identification of glutamic acid 78 as the active site nucleophile in
RT *Bacillus subtilis* xylanase using electrospray tandem mass
RT spectrometry";
RL Biochemistry 33:7027-7032(1994).
CC -!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
CC linkages in xylans.
CC -!- PATHWAY: Xylan degradation.
CC -!- SIMILARITY: Belongs to the glycosyl hydrolase 11 (cellulase G)
CC family.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; M36648; AAA22897.1; -; Genomic DNA.
DR EMBL; AF027868; AAB84458.1; -; Genomic DNA.
DR EMBL; Z99114; CAB13776.1; -; Genomic DNA.
DR PIR; I40569; I40569
DR PDB; 1AXK; X-ray; A/B=-.
DR SMR; P18429; 27-213.
DR Subtilist; BG10808; xyna.
DR InterPro; IPR001137; Glyco_hydro_11.
DR Pfam; PF00457; Glyco_hydro_11; 1.
DR PRINTS; PR00911; GLHYDRLASE11
DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
KW 3D-structure; Complete proteome; Glycosidase; Hydrolase; Signal;
KW Xylan degradation.
FT SIGNAL 1 28
FT CHAIN 29 213 Endo-1,4-beta-xylanase A.
FT ACT SITE 106 106 Nucleophile.
FT ACT SITE 200 200 Proton donor (By similarity).
FT MUTAGEN 106 106 E->S; Dramatically reduced activity.
FT MUTAGEN 200 200 E->S; Dramatically reduced activity.
SQ SEQUENCE 213 AA; 23345 MW; 20CBA35238CC0564 CRC64;

Query Match 100.0%; Score 1171; DB 1; Length 213;
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Matches 213; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MFKEKQFLGLSALMSISLFSATASADYQNMWTDGGGIYNAVNGSGNYSVNWSN 60
Qy 61 TGNFVVGKGTWTPSPFRITNNAGVWAPNGNGYLTLVGWTRSPLEIYVVDVSWGTYRPTG 120
Db 61 TGNFVVGKGTWTPSPFRITNNAGVWAPNGNGYLTLVGWTRSPLEIYVVDVSWGTYRPTG 120
Qy 121 TYKGTVSDGGTYDIYITTRNAPSIDGDRTPFYQWSVROSKRPTGSNATITFSNHVNA 180
Db 121 TYKGTVSDGGTYDIYITTRNAPSIDGDRTPFYQWSVROSKRPTGSNATITFSNHVNA 180
Qy 181 WKSHGMNLGSNWAYQVMWTEGYQSSGSSNVTVM 213

Db 181 WKSHGMNLGSNWAYQVMWTEGYQSSGSSNVTVM 213
RESULT 2
XYNA_BACCI
ID XYNA_BACCI STANDARD; PRT; 213 AA.
AC P09850;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Endo-1,4-beta-xylanase precursor (EC 3.2.1.8) (Xylanase) (1,4-beta-D-
DE xylan xylanohydrolase).
GN Name=xlnA;
OS *Bacillus* Circulans.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; *Bacillus*.
OX NCBI_TaxID=1397;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=88303346; PubMed=3405767;
RA Yang R.C.A., MacKenzie C.R., Narang S.A.;
RT "Nucleotide sequence of a *Bacillus* circulans xylanase gene";
RL Nucleic Acids Res. 16:7187-7187(1988).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS), AND MUTAGENESIS.
RX MEDLINE=94290322; PubMed=8019418;
RA Wakarchuk W.W., Campbell R.L., Sung W.L., Davoodi J., Yaguchi M.;
RT "Mutational and crystallographic analyses of the active site residues
RT of the *Bacillus* circulans xylanase";
RL Protein Sci. 3:467-475(1994).
RN [3]
RP STRUCTURE BY NMR.
RX MEDLINE=96322313; PubMed=8756457; DOI=10.1021/bi9613234;
RA McIntosh L.P., Hand G., Johnson P.E., Joshi M.D., Koerner M.,
RA Plesniak L.A., Ziser L., Wakarchuk W.W., Withers S.G.;
RT "The pKa of the general acid/base carboxyl group of a glycosidase
RT cycles during catalysis: a 13C-NMR study of *Bacillus* circulans
RT xylanase";
RL Biochemistry 35:9958-9966(1996).
CC -!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
CC linkages in xylans.
CC -!- PATHWAY: Xylan degradation.
CC -!- SIMILARITY: Belongs to the glycosyl hydrolase 11 (cellulase G)
CC family.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; X07723; CAA30553.1; -; Genomic DNA.
DR PIR; S01734; S01734.
DR PDB; 1BCX; X-ray; @=29-213.
DR PDB; 1BVV; X-ray; @=29-213.
DR PDB; 1C5H; X-ray; A=29-213.
DR PDB; 1C5I; X-ray; A=29-213.
DR PDB; 1HVO; X-ray; A=29-213.
DR PDB; 1HV1; X-ray; A=29-213.
DR PDB; 1XNB; X-ray; @=29-213.
DR PDB; 1XNC; X-ray; @=29-213.
DR PDB; 2BVV; X-ray; A=29-213.
DR InterPro; IPR001137; Glyco_hydro_11.
DR Pfam; PF00457; Glyco_hydro_11; 1.
DR PRINTS; PR00911; GLHYDRLASE11.
DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
KW 3D-structure; Glycosidase; Hydrolase; Signal; Xylan degradation.
FT SIGNAL 1 28
FT CHAIN 29 213 Endo-1,4-beta-xylanase.
FT ACT SITE 106 106 Nucleophile.
FT ACT SITE 200 200 Proton donor.
FT STRAND 33 38

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FT STRAND 43 48
FT TURN 51 52
FT STRAND 53 59
FT STRAND 63 70
FT TURN 75 76
FT STRAND 78 89
FT STRAND 92 101
FT TURN 102 104
FT STRAND 105 113
FT STRAND 121 128
FT TURN 129 130
FT STRAND 131 140
FT TURN 146 147
FT STRAND 150 160
FT STRAND 170 173
FT STRAND 174 183
FT TURN 184 185
FT STRAND 191 202
FT STRAND 205 213
SQ SEQUENCE 213 AA; 23359 MW; 4BA0A35238CC0135 CRC64;

Query Match 99.7%; Score 1168; DB 1; Length 213;
Best Local Similarity 99.5%; Pred. No. 4e-86;
Matches 212; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFKPKNFVLGLSAAALMSISLFSATASAASTDYWNQWTDGGGINVNAVNGSGGNYVNVNSN 60
DB 1 MFKPKNFVLGLSAAALMSISLFSATASAASTDYWNQWTDGGGINVNAVNGSGGNYVNVNSN 60

QY 61 TGNFVVGKWTGSPFRTINYNAGVWAPNGNGYLTLYGWTRSPLEYYVVDWSWGTYPRTG 120
DB 61 TGNFVVGKWTGSPFRTINYNAGVWAPNGNGYLTLYGWTRSPLEYYVVDWSWGTYPRTG 120

QY 121 TYKGTVKSDGGTYDIYTTTTRYNAPSIDGDRITFTQYWSVRSKRPTGSGNATITFNSHNVA 180
DB 121 TYKGTVKSDGGTYDIYTTTTRYNAPSIDGDRITFTQYWSVRSKRPTGSGNATITFNSHNVA 180

QY 181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTVW 213
DB 181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTVW 213

RESULT 3
Q59254_BACSU
ID Q59254_BACSU PRELIMINARY; PRT; 213 AA.
AC Q59254;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Xylanase (EC 3.2.1.8).
GN Name=xvNA;
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=92140374; PubMed=1310524;
RA Niersbach M., Kreuzaler F., Geerse R.H., Postma P.W., Hirsch H.J.;
RT "Cloning and nucleotide sequence of the Escherichia coli K-12 ppsA
gene, encoding PEP synthase.";
RL Mol. Gen. Genet. 231:332-336(1992).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=168 ttpC2;
RX MEDLINE=95219081; PubMed=7704256;
RA Wolf M., Geczi A., Simon O., Borriass R.;
RT "Genes encoding xylan and beta-glucan hydrolysing enzymes in Bacillus
subtilis: characterization, mapping and construction of strains
deficient in lichenase, cellulase and xylanase.";
RL Microbiology 141:281-290(1995).
RN [3]
RP NUCLEOTIDE SEQUENCE.
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RC STRAIN=168 ttpC2;
RA Borriass R., Wolf M.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z34519; CAA84276.1; -; Genomic_DNA.
DR HSSP; P09850; 1XNB.
DR SMR; Q59254; 27-213.
DR GO; GO:0031176; F:endo-1,4-beta-xylanase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR GO; GO:0045493; P:xylan catabolism; IEA.
DR InterPro; IPR001137; Glyco_hydro_11.
DR Pfam; PF00457; Glyco_hydro_11; 1.
DR PRINTS; PR00911; GLHYDRLASE11.
DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
KW Glycosidase; Hydrolase; Xylan degradation.
SQ SEQUENCE 213 AA; 23355 MW; 21D76D4F8CED4B7 CRC64;

Query Match 99.6%; Score 1166; DB 2; Length 213;
Best Local Similarity 99.5%; Pred. No. 5.8e-86;
Matches 212; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MFKPKNFVLGLSAAALMSISLFSATASAASTDYWNQWTDGGGINVNAVNGSGGNYVNVNSN 60
DB 1 MFKPKNFVLGLSAAALMSISLFSATASAASTDYWNQWTDGGGINVNAVNGSGGNYVNVNSN 60

QY 61 TGNFVVGKWTGSPFRTINYNAGVWAPNGNGYLTLYGWTRSPLEYYVVDWSWGTYPRTG 120
DB 61 TGNFVVGKWTGSPFRTINYNAGVWAPNGNGYLTLYGWTRSPLEYYVVDWSWGTYPRTG 120

QY 121 TYKGTVKSDGGTYDIYTTTTRYNAPSIDGDRITFTQYWSVRSKRPTGSGNATITFNSHNVA 180
DB 121 TYKGTVKSDGGTYDIYTTTTRYNAPSIDGDRITFTQYWSVRSKRPTGSGNATITFNSHNVA 180

QY 181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTVW 213
DB 181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTVW 213

RESULT 4
Q59256_9BACI
ID Q59256_9BACI PRELIMINARY; PRT; 213 AA.
AC Q59256;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Endo-1, 4-beta-xylanase precursor (EC 3.2.1.8).
GN Name=xvNS;
OS Bacillus sp. YA-14.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=72411;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=YA-14;
RA Yu J.H., Park Y.S., Yum D.Y., Kim J.M., Kong I.S., Bai D.H.;
RT "Nucleotide sequence and analysis of a xylanase gene (xvns) from
alkali-tolerant Bacillus sp. YA-14 and comparison with other
xylanases.";
RL J. Microbiol. Biotechnol. 3:139-145(1993).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=YA-14;
RA Hyun Ju Y.;
RL Submitted (DEC-1990) to the EMBL/GenBank/DBJ databases.
DR EMBL; X59058; CAA41783.1; -; Genomic_DNA.
DR PIR; S48126; S48126.
DR HSSP; P09850; 1XNB.
DR SMR; Q59256; 27-213.
DR GO; GO:0031176; F:endo-1,4-beta-xylanase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR GO; GO:0045493; P:xylan catabolism; IEA.
DR InterPro; IPR001137; Glyco_hydro_11.
DR Pfam; PF00457; Glyco_hydro_11; 1.
DR PRINTS; PR00911; GLHYDRLASE11.
```

DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
KW Glycosidase; Hydrolase; Signal; Xylan degradation.
FT SIGNAL 1 28 Potential.
FT CHAIN 29 213 endo-1, 4-beta-xylanase.
SQ SEQUENCE 213 AA; 23341 MW; 2110D35768CC0034 CRC64;

Query Match 99.5%; Score 1165; DB 2; Length 213;
Best Local Similarity 99.1%; Pred. No. 7e-86;
Matches 211; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFKEKKNFLVGLSAAALMSISLFSATASASTDYQNWNTDGGGINVAVNGSGGNSVNWNSN 60
Db 1 MFKEKKNFLVGLSAAALMSISLFSATASASTDYQNWNTDGGGINVAVNGSGGNSVNWNSN 60

Qy 61 TGNFVVGKGTGSPFRTINYNAGWAPNGNGYLYLGYWTRSPLEIYYVVDVSWGTYRPTG 120
Db 61 TGNFVVGKGTGSPFRTINYNAGWAPNGNGYLYLGYWTRSPLEIYYVVDVSWGTYRPTG 120

Qy 121 TYKGTVKSDGTYDIYTTTRYNAPSIDGDRFTTQYWSVRQKPTGNSNATITFSNHVNA 180
Db 121 TYKGTVKSDGTYDIYTTTRYNAPSIDGDRFTTQYWSVRQKPTGNSNATITFSNHVNA 180

Qy 181 WKSHGMNLGSNWAYQVWATEGYQSSGSSNVTW 213
Db 181 WKSHGMNLGSNWAYQVWATEGYQSSGSSNVTW 213

RESULT 5
Q8RMN9_BACSU PRELIMINARY; PRT; 213 AA.
AC Q8RMN9;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Endo-1, 4-xylanase.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RA Sun J., Gu S., Li W., Xiao H., Xiao J., Fu L.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF490979; AAM08359.1; -; Genomic_DNA.
DR HSSP; P09850; 1XNB.
DR SMR; Q8RMN9; 27-213.
DR GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR GO; GO:0045493; P:xylan catabolism; IEA.
DR InterPro; IPR001137; Glyco_hydro_11.
DR Pfam; PF00457; Glyco_hydro_11; 1.
DR PRINTS; PR00911; GLHYDRLASE11.
DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
KW Xylan degradation.
SQ SEQUENCE 213 AA; 23277 MW; 34DFAD4D9C2C0034 CRC64;

Query Match 98.2%; Score 1150; DB 2; Length 213;
Best Local Similarity 98.6%; Pred. No. 1.1e-84;
Matches 210; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MFKEKKNFLVGLSAAALMSISLFSATASASTDYQNWNTDGGGINVAVNGSGGNSVNWNSN 60
Db 1 MFKEKKNFLVGLSAAALMSISLFSATASASTDYQNWNTDGGGINVAVNGSGGNSVNWNSN 60

Qy 61 TGNFVVGKGTGSPFRTINYNAGWAPNGNGYLYLGYWTRSPLEIYYVVDVSWGTYRPTG 120
Db 61 TGNFVVGKGTGSPFRTINYNAGWAPNGNGYLYLGYWTRSPLEIYYVVDVSWGTYRPTG 120

Qy 121 TYKGTVKSDGTYDIYTTTRYNAPSIDGDRFTTQYWSVRQKPTGNSNATITFSNHVNA 180
Db 121 TYKGTVKSDGTYDIYTTTRYNAPSIDGDRFTTQYWSVRQKPTGNSNATITFSNHVNA 180

Qy 181 WKSHGMNLGSNWAYQVWATEGYQSSGSSNVTW 213
Db 181 WKSHGMNLGSNWAYQVWATEGYQSSGSSNVTW 213

RESULT 6
Q8RMN8_BACCI PRELIMINARY; PRT; 213 AA.
AC Q8RMN8;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Endo-1, 4-xylanase.
OS Bacillus circulans.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1397;
RN [1]
RA Sun J., Xu Z., Li W., Gu S., Zhao H., Xiao J., Chen Y.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF490980; AAM08360.1; -; Genomic_DNA.
DR HSSP; P09850; 1XNB.
DR SMR; Q8RMN8; 27-213.
DR GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR GO; GO:0045493; P:xylan catabolism; IEA.
DR InterPro; IPR001137; Glyco_hydro_11.
DR Pfam; PF00457; Glyco_hydro_11; 1.
DR PRINTS; PR00911; GLHYDRLASE11.
DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
KW Xylan degradation.
SQ SEQUENCE 213 AA; 23378 MW; E306B98D49E8CF4D CRC64;

Query Match 97.7%; Score 1144; DB 2; Length 213;
Best Local Similarity 97.7%; Pred. No. 3.4e-84;
Matches 208; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MFKEKKNFLVGLSAAALMSISLFSATASASTDYQNWNTDGGGINVAVNGSGGNSVNWNSN 60
Db 1 MFKEKKNFLVGLSAAALMSISLFSATASASTDYQNWNTDGGGINVAVNGSGGNSVNWNSN 60

Qy 61 TGNFVVGKGTGSPFRTINYNAGWAPNGNGYLYLGYWTRSPLEIYYVVDVSWGTYRPTG 120
Db 61 TGNFVVGKGTGSPFRTINYNAGWAPNGNGYLYLGYWTRSPLEIYYVVDVSWGTYRPTG 120

Qy 121 TYKGTVKSDGTYDIYTTTRYNAPSIDGDRFTTQYWSVRQKPTGNSNATITFSNHVNA 180
Db 121 TYKGTVKSDGTYDIYTTTRYNAPSIDGDRFTTQYWSVRQKPTGNSNATITFSNHVNA 180

Qy 181 WKSHGMNLGSNWAYQVWATEGYQSSGSSNVTW 213
Db 181 WKSHGMNLGSNWAYQVWATEGYQSSGSSNVTW 213

RESULT 7
Q9ZB36_BACSP PRELIMINARY; PRT; 213 AA.
AC Q9ZB36;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Endo-1, 4-beta-xylanhydrolase.
GN Name=xyna;
OS Bacillus sp.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1409;
RN [1]
RA Kim S.C., Jeong K.J., Kim M.S.;
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U51675; AAD10834.1; -; Genomic_DNA.
DR HSSP; P09850; 1XNB.
DR SMR; Q9ZB36; 27-213.

DR	PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; UNKNOWN_1.
DR	PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
KW	Glycosidase; Hydrolase; Signal; Xylan degradation.
FT	SIGNAL 1 29 Potential.
SQ	SEQUENCE 214 AA; 23478 MW; 6FDICB9BB6A5048 CRC64;
Query Match 79.9%; Score 935.5; DB 2; Length 214;	
Best Local Similarity 80.4%; Pred. No. 2.1e-67;	
Matches	172; Conservative 13; Mismatches 28; Indels 1; Gaps 1;
Qy	1 MFPEKKNFLVGLSAAALMS-ISLFSATASASTDYQNWNWDGGIVNAVNGSGGNSYNWS 59
Db	1 MFPLSKKLMLVLLTISMSFISLFTVTAYAASTDYQNWNTDGGGTVNATNGSDGNYSYSWS 60
Qy	60 NTCNFVVVGKGWTGSPFRINTNAGVWPANGCYLTLYGWTRSPLEIYYVVDSWGTVRPT 119
Db	61 NCGNFVVVGKGWTGSATRVINTAGAFSPFGNYGLALYGWTRSLLEYVVDSWGTVRPT 120
Qy	120 GTYKGVTKSDGGTYDIYTTTRYNAPSIDGDRITFTQYWVSQRKRPTGSNATITPSNHVN 179
Db	121 GTYKGVTSDDGYTDIYTTTRTNAPSIDGNITFTQFWSVRQSRPIGTNTTITPSNHVN 180
Qy	180 AWKSHGMNLGSWAYOVMAATEGYQSSGSSNVTVW 213
Db	181 AWKSKGMNLGSSWSYQVLATEGYQSSGYSNVTVW 214
RESULT 12	
XYNA_BACST	
ID_XYNA_BACST	STANDARD; PRT; 210 AA.
AC	P45705;
DT	01-NOV-1995 (Rel. 32, Created)
DT	15-JUL-1998 (Rel. 36, Last sequence update)
DT	10-MAY-2005 (Rel. 47, Last annotation update)
DE	Endo-1,4-beta-xylanase A precursor (EC 3.2.1.8) (Xylanase A) (1,4-
DE	beta-D-xylan xylanhydrolase A).
GN	Name=xynaA.
OS	Bacillus stearothermophilus.
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Geobacillus.
OX	NCBI_TaxId=1422;
RN	[1]
RP	NUTLEOTIDE SEQUENCE.

RESULT 11	
Q6TLP3_9BACT	
ID Q6TLP3_9BACT PRELIMINARY; PRT; 214 AA.	
Q6TLP3;	
AC Q6TLP3;	
DT 05-JUL-2004 (TrEMBLrel. 27, Created)	
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)	
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)	
DE Endo-1,4-beta-xylanase precursor (EC 3.2.1.8).	
OS uncultured bacterium.	
OC Bacteria; environmental samples.	
OX NCBI_TaxID=77133;	
RN [1]	
RP NUCLEOTIDE SEQUENCE.	
RX PubMed=14718652; DOI=10.1110/ps.03333504;	
RA Palackal N., Brennan Y., Callen W.N., Dupree P., Frey G., Goubet F.,	
RA Hazlewood G.P., Healey S., Kang Y.E., Kretz K.A., Lee E., Tan X.,	
RA Tomlinson G.L., Verruto J., Wong V.W.K., Mathur E.J., Short J.M.,	
RA Robertson D.B., Steer B.A.;	
RT "An evolutionary route to xylanase process fitness.";	
RL Protein Sci. 13:494-503(2004).	
DR ENBL; AY394562; AAQ90180.2; -; Genomic_DNA.	
DR HSP; P09850; 1BCX.	
DR SMR; P09850; 1BCX.	
DR SRR; Q6TLP3; 30-214.	
DR GO; GO:0031176; F:endo-1,4-beta-xylanase activity; IEA.	
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.	
DR GO; GO:0045493; P:xylan catabolism; IEA.	
DR InterPro; IPR001137; Glyco hydro 11.	
DR Pfam; PF00457; Glyco hydro 11; 1-	
DR PRINTS; PR00911; GLHYDRASE11.	
DR	
RT "Nucleotide sequence analysis of an endo-xylanase gene (xyrA) from	
RT Bacillus stearothermophilus.";	
RL J. Microbiol. Biotechnol. 5:117-124(1995).	
RN [2]	
RP SEQUENCE REVISION.	
RA Cho S., Choi Y.;	
RA Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.	
RL -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic	
CC linkages in xylans.	
CC -1- PATHWAY: Xylan degradation.	
CC -1- SIMILARITY: Belongs to the glycosyl hydrolase 11 (cellulase G)	
CC family.	
CC	
CC This Swiss-Prot entry is copyright. It is produced through a collaboration	
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -	
CC the European Bioinformatics Institute. There are no restrictions on its	
CC use as long as its content is in no way modified and this statement is not	
CC removed.	
CC	
CC ENBL; U15985; AAB72117.1; -; Genomic_DNA.	
DR HSP; P09850; 1XNB.	
DR SMR; P45705; 24-210.	
DR InterPro; IPR001137; Glyco hydro 11.	
DR Pfam; PF00457; Glyco hydro 11; 1-	
DR PRINTS; PR00911; GLHYDRASE11.	
DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.	
DR PROSITE; PS00777; GLYCOSYL_HYDROL_F12_1; 1.	
DR Glycosidase; Hydrolase; Signal; Xylan degradation.	
DR SIGNAL 1 19 potential.	
FT	

FT CHAIN 20 210 Endo-1,4-beta-xylanase A.
 FT ACT SITE 104 104 Nucleophile (By similarity).
 FT ACT SITE 197 197 Proton donor (By similarity).
 SQ SEQUENCE 210 AA; 23221 MW; 3190CF74C34AAB45 CRC64;

Query Match 79.4%; Score 930; DB 1; Length 210;
 Best Local Similarity 80.6%; Pred. No. 5.6e-67;
 Matches 170; Conservative 11; Mismatches 28; Indels 2; Gaps 2;

QY 3 KFKKFLVGLSAAALMSISLFSATASASTDYQWNTDGGGIYVNAVNGSGNYSVNWSNTG 62
 Db 2 KLKKWLTLLTASMSFGLFGATSSAA--TDYQWNTDGGGMVNAVNGPGNYSVTWQNTG 60

QY 63 NFVVGKWTGSPFFRTINTNAGVWAPNGNGYLTLYGWTRSPLEIYYVVDVSWGTYRPTGY 122
 Db 61 NFVVGKWTGSPNRTINTNAGVWAPNGNGYLTLYGWTRSPLEIYYVVDVSWGTYRPTGY 120

QY 123 KGTVKSDDGTYDIYTTTRYNAPSIDGDRITFTQYWSVRQSKRPTGNSNATITFSNVHNAWK 182
 Db 121 KGTVNSDGGTYDIYTTTRYNAPSIDGDRITFTQYWSVRQSKRPTGNSNATITFSNVHNAWR 179

QY 183 SHGMNLGSSWAVQVWATEGYQSSGSSNVTW 213
 Db 180 SKGMNLGSSWAVQVWATEGYQSSGSSNVTW 210

RESULT 13
 Q43993_AERPU PRELIMINARY; PRT; 211 AA.
 AC Q43993;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Xylanase I precursor.
 GN Name=xynA;
 OS Aeromonas punctata (Aeromonas caviae).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;
 OC Aeromonadaceae; Aeromonas.
 OC NCBI_TaxID=648;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=ME-1; TISSUE=Gut content of silk worm;
 RA Kubota K.B., Suzuki T., Horitsu H., Kawai K., Takamizawa K.;
 RT "Xylanase I of Aeromonas caviae ME-1 isolated from the intestine of a
 RT herbivorous insect (Samia cynthia pyralis).";
 RL Biosci. Biotechnol. Biochem. 56:1463-1464(1992).
 RN [2]

QY 1) of Aeromonas caviae ME-1";
 RC STRAIN=ME-1; TISSUE=Gut content of silk worm;
 RA Suzuki T., Itoh Y., Naito H., Kubota K.B., Horitsu H., Takamizawa K.,
 RA Kawai K.;
 RT "Molecular cloning of the xynA gene encoding an endo-xylanase
 RT 1) of Aeromonas caviae ME-1";
 RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
 DR EMBL; D32065; BAA06837.1; -; Genomic_DNA.
 DR HSSP; P09850; 1XNB.
 DR SMR; Q43993; 25-211.
 DR GO; GO:0004553; P:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
 DR GO; GO:0045493; P:xylan catabolism; IEA.
 DR InterPro; IPR001137; Glyco_hydro_11.
 DR Pfam; PF00457; Glyco_hydro_11; 1.
 DR PRINTS; PR00911; GLYDRLASE1.
 DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; UNKNOWN_1.
 DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
 KW Signal; Xylan degradation.
 FT SIGNAL 1 28 Potential.
 FT CHAIN 29 211 xylanase I.
 SQ SEQUENCE 211 AA; 23136 MW; F9E30403EB935E49 CRC64;

* Query Match 79.3%; Score 929; DB 2; Length 211;
 Best Local Similarity 79.3%; Pred. No. 6.8e-67;
 Matches 169; Conservative 18; Mismatches 24; Indels 2; Gaps 2;

QY 1 MFKFKKFLVGLSAAALMSISLFSATASASTDYQWNTDGGGIYVNAVNGSGNYSVNWSN 60
 Db 1 MFKFKKFLVGLSAAALMSISLFSATASASTDYQWNTDGGGIYVNAVNGSGNYSVNWSN 59

QY 61 TGNFVVGKWTGSPFFRTINTNAGVWAPNGNGYLTLYGWTRSPLEIYYVVDVSWGTYRPTG 120
 Db 60 TGNFVVGKWTGSPNRTINTNAGVWAPNGNGYLTLYGWTRSPLEIYYVVDVSWGTYRPTG 119

QY 121 TYKGTVKSDDGTYDIYTTTRYNAPSIDGDRITFTQYWSVRQSKRPTGNSNATITFSNVHNA 180
 Db 120 TYKGTVNSDGGTYDIYTTTRYNAPSIDGDRITFTQYWSVRQSKRPTGNSNATITFSNVHNA 178

QY 181 WSHGMNLGSSWAVQVWATEGYQSSGSSNVTW 213
 Db 179 WPSKGMNLGSSWAVQVWATEGYQSSGSSNVTW 211

RESULT 14
 Q71S35_BACFI PRELIMINARY; PRT; 210 AA.
 AC Q71S35;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Xylanase.
 OS Bacillus firmus.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OC NCBI_TaxID=1399;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=K-1;
 RA Chuensumran U., Ratanakhanokchai K., Cheevadhanarak S.;
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF317173; AAQ14588.1; -; Genomic_DNA.
 DR HSSP; P09850; 1BCX.
 DR SMR; Q71S35; 27-210.
 DR GO; GO:0004553; P:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
 DR GO; GO:0045493; P:xylan catabolism; IEA.
 DR InterPro; IPR001137; Glyco_hydro_11.
 DR Pfam; PF00457; Glyco_hydro_11; 1.
 DR PRINTS; PR00911; GLYDRLASE1.
 DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
 KW Xylan degradation.
 SQ SEQUENCE 210 AA; 23313 MW; AC4BA5DD5D567A1B2 CRC64;

Query Match 73.8%; Score 864.5; DB 2; Length 210;
 Best Local Similarity 74.2%; Pred. No. 1.1e-61;
 Matches 158; Conservative 19; Mismatches 33; Indels 3; Gaps 2;

QY 1 MFKFKKFLVGLSAAALMSISLFSATASASTDYQWNTDGGGIYVNAVNGSGNYSVNWSN 60
 Db 1 MFKFKKFLVGLSAAALMSISLFSATASASTDYQWNTDGGGIYVNAVNGSGNYSVNWSN 58

QY 61 TGNFVVGKWTGSPFFRTINTNAGVWAPNGNGYLTLYGWTRSPLEIYYVVDVSWGTYRPTG 120
 Db 59 TGNFVVGKWTGSPNRTINTNAGVWAPNGNGYLTLYGWTRSPLEIYYVVDVSWGTYRPTG 118

QY 121 TYKGTVKSDDGTYDIYTTTRYNAPSIDGDRITFTQYWSVRQSKRPTGNSNATITFSNVHNA 180
 Db 119 THRGTVNSDGGTYDIYTTTRYNAPSIDGDRITFTQYWSVRQSKRPTGNSNATITFSNVHNA 177

QY 181 WSHGMNLGSSWAVQVWATEGYQSSGSSNVTW 213
 Db 178 WRNAGMNLGSSWAVQVWATEGYQSSGSSNVTW 210

RESULT 15
 Q9KEF3_BACHD PRELIMINARY; PRT; 210 AA.
 AC Q9KEF3;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)

Search completed: February 3, 2006, 09:12:20
Job time : 249 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 3, 2006, 09:11:33 ; Search time 28 Seconds
(without alignments)
628.926 Million cell updates/sec

Title: US-10-626-724-5
Perfect score: 1171
Sequence: 1 MFKFKNPLVGLSALMSIS.....YQVMATEGYQSSGSSNVTW 213

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA*
1: /cgn2_6/ptodata/1/1aa/5 COMB.pcp.*
2: /cgn2_6/ptodata/1/1aa/6 COMB.pcp.*
3: /cgn2_6/ptodata/1/1aa/H COMB.pcp.*
4: /cgn2_6/ptodata/1/1aa/pCTUS COMB.pcp.*
5: /cgn2_6/ptodata/1/1aa/RE COMB.pcp.*
6: /cgn2_6/ptodata/1/1aa/backfiles.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1168	99.7	213	2	US-09-570-856B-1 Sequence 1, Appli
2	1168	99.7	213	2	US-09-570-856B-13 Sequence 13, Appli
3	1141	97.4	208	1	US-08-315-695-21 Sequence 21, Appli
4	1130	96.5	213	1	US-08-104-445-3 Sequence 3, Appli
5	1041	88.9	185	1	US-08-044-621D-37 Sequence 37, Appli
6	1041	88.9	185	1	US-08-709-912-5 Sequence 5, Appli
7	1041	88.9	185	1	US-09-047-370-5 Sequence 5, Appli
8	1038	88.6	185	1	US-08-044-621D-36 Sequence 36, Appli
9	1038	88.6	185	1	US-08-709-912-3 Sequence 3, Appli
10	1038	88.6	185	1	US-09-047-370-3 Sequence 3, Appli
11	987	84.3	185	2	US-09-570-856B-5 Sequence 5, Appli
12	984	84.0	185	2	US-09-570-856B-9 Sequence 9, Appli
13	979	83.6	185	2	US-09-570-856B-7 Sequence 7, Appli
14	977	83.4	185	2	US-09-570-856B-4 Sequence 4, Appli
15	976	83.3	185	2	US-09-570-856B-6 Sequence 6, Appli
16	974	83.2	185	2	US-09-570-856B-3 Sequence 3, Appli
17	955	81.6	185	2	US-09-570-856B-10 Sequence 10, Appli
18	955	81.6	211	1	US-08-575-964-1 Sequence 1, Appli
19	955	81.6	211	1	US-08-963-500-1 Sequence 1, Appli
20	951	81.2	185	2	US-09-570-856B-12 Sequence 12, Appli
21	933	79.7	185	2	US-09-570-856B-8 Sequence 8, Appli
22	920	78.6	185	2	US-09-570-856B-11 Sequence 11, Appli
23	640.5	54.7	189	1	US-08-709-912-13 Sequence 13, Appli
24	640.5	54.7	189	1	US-09-047-370-13 Sequence 13, Appli
25	637	54.4	240	2	US-09-570-856B-16 Sequence 16, Appli
26	636	54.3	344	1	US-08-468-812-2 Sequence 2, Appli
27	636	54.3	344	2	US-08-590-563-2 Sequence 2, Appli

28	636	54.3	344	2	US-09-770-621-2	Sequence 2, Appli
29	636	54.3	344	2	US-09-235-832-2	Sequence 2, Appli
30	635	54.2	216	1	US-08-315-695-20	Sequence 20, Appli
31	627.5	53.6	200	1	US-07-744-570B-2	Sequence 2, Appli
32	625.5	53.4	191	1	US-08-044-621D-35	Sequence 35, Appli
33	618.5	52.8	191	1	US-08-709-912-11	Sequence 11, Appli
34	618.5	52.8	191	1	US-09-047-370-11	Sequence 11, Appli
35	594	50.7	206	1	US-08-315-695-19	Sequence 19, Appli
36	594	50.7	215	1	US-08-044-621D-34	Sequence 34, Appli
37	594	50.7	335	2	US-09-570-856B-15	Sequence 15, Appli
38	587	50.1	191	1	US-08-709-912-10	Sequence 10, Appli
39	587	50.1	191	1	US-09-047-370-10	Sequence 10, Appli
40	585.5	50.0	230	2	US-08-768-373-4	Sequence 4, Appli
41	585.5	50.0	230	2	US-09-849-242A-4	Sequence 4, Appli
42	583.5	49.8	225	1	US-08-290-979A-8	Sequence 8, Appli
43	579	49.4	189	1	US-08-044-621D-33	Sequence 33, Appli
44	573.5	49.0	225	2	US-09-570-856B-26	Sequence 26, Appli
45	572	48.8	189	1	US-08-709-912-12	Sequence 12, Appli

ALIGNMENTS

RESULT 1
US-09-570-856B-1
; Sequence 1, Application US/09570856B
; Patent No. 6682923
; GENERAL INFORMATION:
; APPLICANT: Bentzien, Joerg M
; APPLICANT: Dahiyat, Basil I
; TITLE OF INVENTION: NOVEL THERMOSTABLE ALKALIPHILIC XYLANASE
; FILE REFERENCE: A-67478-1/RFT/RMS/RMK
; CURRENT APPLICATION NUMBER: US/09/570.856B
; CURRENT FILING DATE: 2002-04-15
; PRIOR APPLICATION NUMBER: US 60/133,714
; PRIOR FILING DATE: 1999-05-12
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 1
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Bacillus circulans
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)..(28)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (29)..()
; OTHER INFORMATION:
US-09-570-856B-1

Query Match 99.7%; Score 1168; DB 2; Length 213;
Best Local Similarity 99.5%; Pred. No. 6.3e-98;
Matches 212; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MFKFKNPLVGLSALMSISLFSATASAASTDYQWNTDGGGIYVAVNGSGNYSVWNSN 60
Db 1 MFKFKNPLVGLSALMSISLFSATASAASTDYQWNTDGGGIYVAVNGSGNYSVWNSN 60
QY 61 TGNFVVGKWTGTPPRTINTNAGVWAPNGNGYLYLYGWTRSPLEYVYVDSWGTYPGTG 120
Db 61 TGNFVVGKWTGTPPRTINTNAGVWAPNGNGYLYLYGWTRSPLEYVYVDSWGTYPGTG 120
QY 121 TYKGTVKSDDGTYYIYTTTTRYNAPSIDGDRFTTQYWSVRSKRPTGSGNATITFSHNVA 180
Db 121 TYKGTVKSDDGTYYIYTTTTRYNAPSIDGDRFTTQYWSVRSKRPTGSGNATITFSHNVA 180
QY 181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTW 213
Db 181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTW 213

RESULT 2

US-09-570-856B-13
; Sequence 13, Application US/09570856B
; Patent No. 6682923
; GENERAL INFORMATION:
; APPLICANT: Bentzien, Joerg M
; APPLICANT: Dahiyat, Bassil I
; TITLE OF INVENTION: NOVEL THERMOSTABLE ALKALIPHILIC XYLANASE
; FILE REFERENCE: A-67478-1/RFT/RMS/RMK
; CURRENT APPLICATION NUMBER: US/09/570,856B
; CURRENT FILING DATE: 2002-04-15
; PRIOR APPLICATION NUMBER: US 60/133,714
; PRIOR FILING DATE: 1999-05-12
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Bacillus subtilis
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)..(28)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (29)..()
; OTHER INFORMATION:
; US-09-570-856B-13

Query Match 99.7%; Score 1168; DB 2; Length 213;

Best Local Similarity 99.5%; Pred. No. 6.3e-98;

Matches 212; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MFKFKNPLVGLSALMSISLFSATASASTDYQWNTDGGGINVAVNGSGGNTSVNWSN	60
Db	1	MFKFKNPLVGLSALMSISLFSATASASTDYQWNTDGGGINVAVNGSGGNTSVNWSN	60
Qy	61	TGNFVVGKWTGSPFRITINAGVWAPNGNGYLTLYGWTSPLEIYYVVDWSGTYRPTG	120
Db	61	TGNFVVGKWTGSPFRITINAGVWAPNGNGYLTLYGWTSPLEIYYVVDWSGTYRPTG	120
Qy	121	TYKGTVKSDDGTYDIYITRYNAPSIDGDRITFTQYWSVRQSKRPTGSNATITFSNVNA	180
Db	121	TYKGTVKSDDGTYDIYITRYNAPSIDGDRITFTQYWSVRQSKRPTGSNATITFSNVNA	180
Qy	181	WKSNGMLGSNWAYQVMATEGYQSSGSSNVTVW	213
Db	181	WKSNGMLGSNWAYQVMATEGYQSSGSSNVTVW	213

RESULT 3

US-08-315-695-21
; Sequence 21, Application US/08315695
; Patent No. 5591619
; GENERAL INFORMATION:
; APPLICANT: Li, Xin-Liang
; APPLICANT: Ljungdahl, Lars G.
; TITLE OF INVENTION: Aureobasidium Pullulans Xylanase, Gene
; TITLE OF INVENTION: and Signal Sequence
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee and Winner, P.C.
; STREET: 5370 Manhattan Circle, Suite 201
; CITY: Boulder
; STATE: CO
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/315,695
; FILING DATE: 30-SEP-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Winner, Ellen P.
; REGISTRATION NUMBER: 28,547
; REFERENCE/DOCKET NUMBER: 55-94
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 499-8080
; TELEFAX: (303) 499-8089
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 208 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; US-08-315-695-21

Query Match 97.4%; Score 1141; DB 1; Length 208;

Best Local Similarity 99.5%; Pred. No. 1.7e-95;

Matches 207; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy	6	KNFLVGLSALMSISLFSATASASTDYQWNTDGGGINVAVNGSGGNTSVNWSNTGNFV	65
Db	1	KNFLVGLSALMSISLFSATASASTDYQWNTDGGGINVAVNGSGGNTSVNWSNTGNFV	60
Qy	66	VGKGTWTGSPFRITINAGVWAPNGNGYLTLYGWTSPLEIYYVVDWSGTYRPTGYKGT	125
Db	61	VGKGTWTGSPFRITINAGVWAPNGNGYLTLYGWTSPLEIYYVVDWSGTYRPTGYKGT	120
Qy	126	VKSDGGTYDIYITRYNAPSIDGDRITFTQYWSVRQSKRPTGSNATITFSNVNAWKSHG	185
Db	121	VKSDGGTYDIYITRYNAPSIDGDRITFTQYWSVRQSKRPTGSNATITFTNVNAWKSHG	180
Qy	186	MNLGSNWAYQVMATEGYQSSGSSNVTVW	213
Db	181	MNLGSNWAYQVMATEGYQSSGSSNVTVW	208

RESULT 4

US-08-104-445-3

; Sequence 3, Application 08/104445

; Patent No. 5306633

; GENERAL INFORMATION:

; APPLICANT: GOTTSCHALK, MICHAEL

; APPLICANT: SCHUSTER, ERWIN

; APPLICANT: SPROESSLER, BRUNO

; TITLE OF INVENTION: BACTERIAL XYLANASE, METHOD FOR ITS

; TITLE OF INVENTION: PRODUCTION, BACTERIA PRODUCING A XYLANASE, DNA FRAGMENT

; TITLE OF INVENTION: ENCODING A XYLANASE, PLASMID CONTAINING THE DNA FRAGMENT,

; TITLE OF INVENTION: BAKING AGENTS CONTAINING A XYLANASE, AND METHOD FO

; NUMBER OF SEQUENCES: 3

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,

; ADDRESSEE: P.C.

; STREET: 1755 S. Jefferson Davis Highway, Suite 400

; CITY: Arlington

; STATE: Virginia

; COUNTRY: U.S.A.

; ZIP: 22202

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: 08/104,445

; FILING DATE:

; CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: ODLON, No. 5306633man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 583-179-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 213 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-104-445-3

Query Match 96.5%; Score 1130; DB 1; Length 213;
Best Local Similarity 95.3%; Pred. No. 1.7e-94;
Matches 203; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 MFKPKKFLVGLSALMSISLFSATASAASTDYQWQNTDGGGINVAVNGSGGNYSVNWSN 60
Db 1 MFKPKKFLVGLTAAFMSISMFSAATAAGTDYQWQNTDGGGINVAVNGSGGNYSVNWSN 60

QY 61 TGNFVVGKGTGSPFRINTYVAVNGWAPNGNGLYLYGWTRSPLEIYYVVDVSWGTYRPTG 120
Db 61 TGNFVVGKGTGSPFRINTYVAVNGWAPNGNGLYLYGWTRSPLEIYYVVDVSWGTYRPTG 120

QY 121 TYKGTVKSDGGTYDIYTTTRYNAPSIDGDRFTTQYWSVROSKRPTGSGNATITFSNHVNA 180
Db 121 TYKGTVKSDGGTYDIYTTTRYNAPSIDGDRFTTQYWSVROSKRPTGSGNATITFSNHVNA 180

QY 181 WKSHGMNLSNWAYQVMALEGYQSSGSSNVTVM 213
Db 181 WKSHGMNLSNWAYQVMALEGYQSSGSSNVTVM 213

RESULT 5
US-08-044-621D-37
Sequence 37, Application US/08044621D
Patent No. 5405769
GENERAL INFORMATION:
APPLICANT: Warren W. Wakarchuk
APPLICANT: Wing L. Sung
APPLICANT: Makoto Yaguchi
APPLICANT: Robert L. Campbell
APPLICANT: David R. Rose
TITLE OF INVENTION: CONSTRUCTION OF THERMOSTABLE MUTANTS
TITLE OF INVENTION: OF A LOW MOLECULAR MASS XYLANASE
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Gowing, Strathy & Henderson
STREET: Suite 2600, 160 Elgin Street
CITY: Ottawa
STATE: Ontario
COUNTRY: Canada
ZIP: K1P 1C3
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 in., 360KB storage
COMPUTER: IBM PC
OPERATING SYSTEM: PC-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/044,621D
FILING DATE: April 8, 1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Judy A. Erratt
REGISTRATION NUMBER: 34,076
REFERENCE/DOCKET NUMBER: 08-863796

TELECOMMUNICATION INFORMATION:
TELEPHONE: 613-786-0199
TELEFAX: 613-563-9869
TELEX:
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 185
TYPE: Amino Acid
STRANDEDNESS: No. 5405769 Relevant
TOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION: protein
HYPOTHETICAL: No
ANTI-SENSE: No
FRAGMENT TYPE: No
ORIGINAL SOURCE:
ORGANISM: Bacillus subtilis
IMMEDIATE SOURCE:
POSITION IN GENOME:
FEATURE:
PUBLICATION INFORMATION:
AUTHORS: Paice M.G., Bourbonnais R., Desrochers
AUTHORS: M., Jurasek L., & Yaguchi M.
TITLE:
JOURNAL: Arch. Microbiol.
VOLUME: 144
ISSUE:
PAGES: 201-206
DATE: 1986
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-044-621D-37

Query Match 88.9%; Score 1041; DB 1; Length 185;
Best Local Similarity 100.0%; Pred. No. 1.6e-86;
Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 ASTDYQWQNTDGGGINVAVNGSGGNYSVNWSNTGNFVVGKGTGSPRTTINYNAGVWAP 88
Db 1 ASTDYQWQNTDGGGINVAVNGSGGNYSVNWSNTGNFVVGKGTGSPRTTINYNAGVWAP 60

QY 89 NNGYLYLYGWTRSPLEIYYVVDVSWGTYRPTGTYKGTVKSDGGTYDIYTTTRYNAPSIDG 148
Db 61 NNGYLYLYGWTRSPLEIYYVVDVSWGTYRPTGTYKGTVKSDGGTYDIYTTTRYNAPSIDG 120

QY 149 DRTTFTQYWSVROSKRPTGSGNATITFSNHVNAWKSHGMNLSNWAYQVMALEGYQSSGSS 208
Db 121 DRTTFTQYWSVROSKRPTGSGNATITFSNHVNAWKSHGMNLSNWAYQVMALEGYQSSGSS 180

QY 209 NVTVM 213
Db 181 NVTVM 185

RESULT 6
US-08-709-912-5
Sequence 5, Application US/08709912
Patent No. 5759840
GENERAL INFORMATION:
APPLICANT: Sung Dr., Wing L
APPLICANT: Yaguchi Dr., Makoto
APPLICANT: Ishikawa Dr., Kazuhiko
TITLE OF INVENTION: Modification of Xylanase to Improve
TITLE OF INVENTION: Thermophilicity, Alkalophilicity and
TITLE OF INVENTION: Thermostability
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fitzpatrick, Cella, Harper, and Scinto
STREET: 277 Park Ave.
CITY: New York
STATE: New York

COUNTRY: USA
ZIP: 10172-0194
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/709,912
FILING DATE: 09-SEP-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Olsen Mr, Warren E
REGISTRATION NUMBER: 27290
REFERENCE/DOCKET NUMBER: 1039.2000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-2400
TELEFAX: (212) 758-2982
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 185 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Bacillus subtilus
PUBLICATION INFORMATION:
AUTHORS: Parce, M.G.
AUTHORS: Bourbonnais, R
AUTHORS: Desrochers, M
AUTHORS: Jurasek, L
AUTHORS: Yaguchi, M
JOURNAL: Arch. Microbiol.
VOLUME: 144
PAGES: 201-206
DATE: 1986

TITLE OF INVENTION: Thermostability
 NUMBER OF SEQUENCES: 54
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fitzpatrick, Cella, Harper, and Scinto
 STREET: 277 Park Ave.
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10172-0194
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/047,370
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/709,912
 FILING DATE: 09-SEP-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Olsen Mr, Warren E
 REGISTRATION NUMBER: 27290
 REFERENCE/DOCKET NUMBER: 1039-2000
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 758-2400
 TELEFAX: (212) 758-2982
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 185 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE: internal
 ORIGINAL SOURCE:
 ORGANISM: Bacillus subtilus
 PUBLICATION INFORMATION:
 AUTHORS: Parce, M.G.
 AUTHORS: Bourbonnais, R
 AUTHORS: Desrochers, M
 AUTHORS: Jurasek, L
 AUTHORS: Yaguchi, M
 JOURNAL: Arch. Microbiol.
 VOLUME: 144
 PAGES: 201-206
 DATE: 1986

RESULT 7
US-09-047-370-5
; Sequence 5, Application US/09047370
; Patent No. 5865408
; GENERAL INFORMATION:
; APPLICANT: Sung Dr., Wing L
; APPLICANT: Yaguchi Dr., Makoto
; APPLICANT: Ishikawa Dr., Kazuhiko
; TITLE OF INVENTION: Modification of Xylanase to Improve
; TITLE OF INVENTION: Thermophilicity, Alkalophilicity and
; TITLE OF INVENTION: Thermophilicity, Alkalophilicity and


```
Db 181 NVTW 185

RESULT 12
US-09-570-856B-9
; Sequence 9, Application US/09570856B
; Patent No. 6682923
; GENERAL INFORMATION:
; APPLICANT: Bentzien, Joerg M
; APPLICANT: Dahiyat, Bassil I
; TITLE OF INVENTION: NOVEL THERMOSTABLE ALKALIPHILIC XYLANASE
; FILE REFERENCE: A-67478-1/RFT/RMS/RMK
; CURRENT APPLICATION NUMBER: US/09/570,856B
; PRIOR FILING DATE: 2002-04-15
; PRIOR APPLICATION NUMBER: US 60/133,714
; PRIOR FILING DATE: 1999-05-12
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-09-570-856B-9

Query Match 84.0%; Score 984; DB 2; Length 185;
Best Local Similarity 93.5%; Pred. No. 2.3e-81;
Matches 173; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

Qy 29 ASTDYWQNTDGGGIVNAVNGSGGNYSVNWSNTGNFVVGKGTGTTGSPRTTINYNAGWAP 88
Db 1 ASTDYWQNTDGGGIVNAVNGSGGNYSVNWSNTGNFVVGKGTGTTGSPRTTINYNAGWAP 60

Qy 89 NNGVLTLYGWTRSPLEIYYVVDWSGTYRPTGTYKGTGTVKSDGGTYDIYTTTRYNAPSIDG 148
Db 61 NNGVLTLYGWTRSPLEIYYVVDWSGTYRPTGTYKGTGTVKSDGGTYDIYTTTRYNAPSIDG 120

Qy 149 DRTTFTQYWSVRQSKRPTGNSNATITFSNHNVAWSKSHGNLGSNNWAYQVMATEGYQSSGSS 208
Db 121 DRTTFTQYWSVRQSKRPTGNSNATITFSNHNVAWSKSHGNLGSNNWAYQVMATEGYQSSGSS 180

Qy 209 NVTW 213
Db 181 NVTW 185

RESULT 13
US-09-570-856B-7
; Sequence 7, Application US/09570856B
; Patent No. 6682923
; GENERAL INFORMATION:
; APPLICANT: Bentzien, Joerg M
; APPLICANT: Dahiyat, Bassil I
; TITLE OF INVENTION: NOVEL THERMOSTABLE ALKALIPHILIC XYLANASE
; FILE REFERENCE: A-67478-1/RFT/RMS/RMK
; CURRENT APPLICATION NUMBER: US/09/570,856B
; PRIOR FILING DATE: 2002-04-15
; PRIOR APPLICATION NUMBER: US 60/133,714
; PRIOR FILING DATE: 1999-05-12
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-09-570-856B-7

Query Match 83.6%; Score 979; DB 2; Length 185;
Best Local Similarity 94.1%; Pred. No. 6.5e-81;
Matches 174; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Qy 29 ASTDYWQNTDGGGIVNAVNGSGGNYSVNWSNTGNFVVGKGTGTTGSPRTTINYNAGWAP 88
Db 1 ASTDYWQNTDGGGIVNAVNGSGGNYSVNWSNTGNFVVGKGTGTTGSPRTTINYNAGWAP 60

Qy 89 NNGVLTLYGWTRSPLEIYYVVDWSGTYRPTGTYKGTGTVKSDGGTYDIYTTTRYNAPSIDG 148
Db 61 NNGVLTLYGWTRSPLEIYYVVDWSGTYRPTGTYKGTGTVKSDGGTYDIYTTTRYNAPSIDG 120

Qy 149 DRTTFTQYWSVRQSKRPTGNSNATITFSNHNVAWSKSHGNLGSNNWAYQVMATEGYQSSGSS 208
Db 121 DRTTFTQYWSVRQSKRPTGNSNATITFSNHNVAWSKSHGNLGSNNWAYQVMATEGYQSSGSS 180

Qy 209 NVTW 213
Db 181 NVTW 185

RESULT 14
US-09-570-856B-4
; Sequence 4, Application US/09570856B
; Patent No. 6682923
; GENERAL INFORMATION:
; APPLICANT: Bentzien, Joerg M
; APPLICANT: Dahiyat, Bassil I
; TITLE OF INVENTION: NOVEL THERMOSTABLE ALKALIPHILIC XYLANASE
; FILE REFERENCE: A-67478-1/RFT/RMS/RMK
; CURRENT APPLICATION NUMBER: US/09/570,856B
; PRIOR FILING DATE: 2002-04-15
; PRIOR APPLICATION NUMBER: US 60/133,714
; PRIOR FILING DATE: 1999-05-12
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-09-570-856B-4

Query Match 83.4%; Score 977; DB 2; Length 185;
Best Local Similarity 94.1%; Pred. No. 9.8e-81;
Matches 174; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

Qy 29 ASTDYWQNTDGGGIVNAVNGSGGNYSVNWSNTGNFVVGKGTGTTGSPRTTINYNAGWAP 88
Db 1 ASTDYWQNTDGGGIVNAVNGSGGNYSVNWSNTGNFVVGKGTGTTGSPRTTINYNAGWAP 60

Qy 89 NNGVLTLYGWTRSPLEIYYVVDWSGTYRPTGTYKGTGTVKSDGGTYDIYTTTRYNAPSIDG 148
Db 61 NNGVLTLYGWTRSPLEIYYVVDWSGTYRPTGTYKGTGTVKSDGGTYDIYTTTRYNAPSIDG 120

Qy 149 DRTTFTQYWSVRQSKRPTGNSNATITFSNHNVAWSKSHGNLGSNNWAYQVMATEGYQSSGSS 208
Db 121 DRTTFTQYWSVRQSKRPTGNSNATITFSNHNVAWSKSHGNLGSNNWAYQVMATEGYQSSGSS 180

Qy 209 NVTW 213
Db 181 NVTW 185

RESULT 15
US-09-570-856B-6
; Sequence 6, Application US/09570856B
; Patent No. 6682923
; GENERAL INFORMATION:
; APPLICANT: Bentzien, Joerg M
; APPLICANT: Dahiyat, Bassil I
; TITLE OF INVENTION: NOVEL THERMOSTABLE ALKALIPHILIC XYLANASE
; FILE REFERENCE: A-67478-1/RFT/RMS/RMK
; CURRENT APPLICATION NUMBER: US/09/570,856B
; PRIOR FILING DATE: 2002-04-15
```


GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 3, 2006, 09:12:33 ; Search time 8 Seconds
(without alignments)
311.993 Million cell updates/sec

Title: US-10-626-724-5

Perfect score: 1171

Sequence: 1 MFKFKNFLVGLSAAALMSIS.....YQNMATEGYQSSGNVTW 213

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 88029 seqs, 11718060 residues

Total number of hits satisfying chosen parameters: 88029

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA-New:

1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pap.*
2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pap.*
3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pap.*
4: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pap.*
5: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pap.*
6: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pap.*
7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pap.*
8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1171	100.0	213	6	US-10-517-939-188
2	1171	100.0	213	7	US-11-170-653-16
3	1168	99.7	213	6	US-10-517-939-224
4	1168	99.7	213	7	US-11-170-653-17
5	1104	94.3	213	6	US-10-517-939-230
6	1097	93.7	213	6	US-10-517-939-302
7	1041	88.9	185	7	US-11-170-653-1
8	933.5	79.7	214	6	US-10-517-939-198
9	933.5	79.7	214	6	US-10-517-939-158
10	929	79.3	211	7	US-11-170-653-19
11	927	79.2	210	6	US-10-517-939-208
12	907.5	77.5	211	7	US-11-170-653-18
13	886	75.7	189	6	US-10-517-939-190
14	873.5	74.6	184	6	US-10-517-939-252
15	844	72.1	189	6	US-10-517-939-380
16	834	71.2	189	6	US-10-517-939-378
17	826	70.5	189	6	US-10-517-939-376
18	710	60.6	222	6	US-10-517-939-168
19	687	58.7	445	6	US-10-517-939-368
20	669.5	57.2	225	6	US-10-517-939-172
21	663.5	56.7	241	7	US-11-170-653-43
22	659	56.3	240	7	US-11-170-653-42
23	658	56.2	361	6	US-10-517-939-212
24	647.5	55.3	355	6	US-10-517-939-206
25	646	55.2	242	7	US-11-170-653-41

ALIGNMENTS

RESULT 1

US-10-517-939-188

; Sequence 188, Application US/10517939

; Publication No. US20060003433A1

; GENERAL INFORMATION:

; APPLICANT: Steer, Brian

; APPLICANT: Callen, Walter

; APPLICANT: Healey, Shaun

; APPLICANT: Hazlewood, Geoff

; APPLICANT: Wu, Di

; APPLICANT: Blum, David

; APPLICANT: Esteghalian, Alireza

; TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING THEM

; AND METHODS FOR MAKING AND USING THEM

; FILE REFERENCE: 564462007901

; CURRENT APPLICATION NUMBER: US/10/517,939

; CURRENT FILING DATE: 2004-12-13

; PRIOR APPLICATION NUMBER: PCT/US03/19153

; PRIOR FILING DATE: 2003-06-16

; PRIOR APPLICATION NUMBER: 60/389,299

; PRIOR FILING DATE: 2002-06-14

; NUMBER OF SEQ ID NOS: 380

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 188

; LENGTH: 213

; TYPE: PRT

; ORGANISM: Unknown

; FEATURE:

; OTHER INFORMATION: Obtained from an environmental sample

; FEATURE:

; NAME/KEY: SIGNAL

; LOCATION: (1)...(28)

US-10-517-939-188

Query Match 100.0%; Score 1171; DB 6; Length 213;

Best Local Similarity 100.0%; Pred. No. 7.6e-96;

Matches 213; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFKFKNFLVGLSAAALMSISLFSATASAASDYQNMWDGGLVNVNNGSGNYSVWNSN 60

Db 1 MFKFKNFLVGLSAAALMSISLFSATASAASDYQNMWDGGLVNVNNGSGNYSVWNSN 60

Qy 61 TGNFVVGKWTGSPFRTINYNAGVWAPNGVLYLYGWTSPLEIYVVDVSWGTYRPTG 120

Db 61 TGNFVVGKWTGSPFRTINYNAGVWAPNGVLYLYGWTSPLEIYVVDVSWGTYRPTG 120

Qy 121 TYKGTVSKDGTGYDIYITTRYNAPSIDGDRPTTQYVSVROSQKPTGSAITTSNHNVA 180

Db 121 TYKGTVSKDGTGYDIYITTRYNAPSIDGDRPTTQYVSVROSQKPTGSAITTSNHNVA 180

Db 121 TYKGTAKSDGGTYDIYTTTTRYNAPSIDGDRTTFTQYMSVRSQSKRPTGNSNATITFSNHVNA 180

Qy 181 WKSHGMNLGSNWAYQVWATEGYQSSGSSNVTW 213

Db 181 WKSHGMNLGSNWAYQVWATEGYQSSGSSNVTW 213

RESULT 2

US-11-170-653-16

; Sequence 16, Application US/11170653

; Publication No. US20050271769A1

; GENERAL INFORMATION:

; APPLICANT: Danisco A/S

; APPLICANT: Sibbesen, Ole

; APPLICANT: Sorensen, Jens

; TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor

; FILE REFERENCE: 674509-2046

; CURRENT APPLICATION NUMBER: US/11/170,653

; CURRENT FILING DATE: 2005-06-23

; PRIOR FILING DATE: US/10/237,386

; PRIOR FILING DATE: 2002-09-09

; PRIOR APPLICATION NUMBER: PCT/IB01/00426

; PRIOR FILING DATE: 2001-03-08

; PRIOR APPLICATION NUMBER: GB 0005585.5

; PRIOR FILING DATE: 2000-03-08

; PRIOR APPLICATION NUMBER: GB 0015751.1

; PRIOR FILING DATE: 2000-06-27

; NUMBER OF SEQ ID NOS: 66

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 16

; LENGTH: 213

; TYPE: PRT

; ORGANISM: Bacillus subtilis

US-11-170-653-16

Query Match 100.0%; Score 1171; DB 7; Length 213;

Best Local Similarity 100.0%; Pred. No. 7.6e-96;

Matches 213; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFKFKQKFLVGLSAAALMSISLFSATASASTDYQWNTDGGIYNAVNGSGGNSVNWNS 60

Db 1 MFKFKQKFLVGLSAAALMSISLFSATASASTDYQWNTDGGIYNAVNGSGGNSVNWNS 60

Qy 61 TGNFVVGKGTGSPFRTINYNAGVWAPNGNGYLTLYGWTRSPLIEYYVVDWSWGTYRPTG 120

Db 61 TGNFVVGKGTGSPFRTINYNAGVWAPNGNGYLTLYGWTRSPLIEYYVVDWSWGTYRPTG 120

Qy 121 TYKGTAKSDGGTYDIYTTTTRYNAPSIDGDRTTFTQYMSVRSQSKRPTGNSNATITFSNHVNA 180

Db 121 TYKGTAKSDGGTYDIYTTTTRYNAPSIDGDRTTFTQYMSVRSQSKRPTGNSNATITFSNHVNA 180

Qy 181 WKSHGMNLGSNWAYQVWATEGYQSSGSSNVTW 213

Db 181 WKSHGMNLGSNWAYQVWATEGYQSSGSSNVTW 213

RESULT 3

US-10-517-939-224

; Sequence 224, Application US/10517939

; Publication No. US20060003433A1

; GENERAL INFORMATION:

; APPLICANT: Steer, Brian

; APPLICANT: Callen, Walter

; APPLICANT: Healey, Shaun

; APPLICANT: Hazlewood, Geoff

; APPLICANT: Wu, Di

; APPLICANT: Blum, David

; APPLICANT: Esegblalian, Alireza

; TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING THEM

; FILE REFERENCE: 564462007901

; CURRENT APPLICATION NUMBER: US/10/517,939

; CURRENT FILING DATE: 2004-12-13

Qy 1 MFKFKQKFLVGLSAAALMSISLFSATASASTDYQWNTDGGIYNAVNGSGGNSVNWNS 60

Db 1 MFKFKQKFLVGLSAAALMSISLFSATASASTDYQWNTDGGIYNAVNGSGGNSVNWNS 60

Qy 61 TGNFVVGKGTGSPFRTINYNAGVWAPNGNGYLTLYGWTRSPLIEYYVVDWSWGTYRPTG 120

Db 61 TGNFVVGKGTGSPFRTINYNAGVWAPNGNGYLTLYGWTRSPLIEYYVVDWSWGTYRPTG 120

Qy 121 TYKGTAKSDGGTYDIYTTTTRYNAPSIDGDRTTFTQYMSVRSQSKRPTGNSNATITFSNHVNA 180

Db 121 TYKGTAKSDGGTYDIYTTTTRYNAPSIDGDRTTFTQYMSVRSQSKRPTGNSNATITFSNHVNA 180

Qy 181 WKSHGMNLGSNWAYQVWATEGYQSSGSSNVTW 213

Db 181 WKSHGMNLGSNWAYQVWATEGYQSSGSSNVTW 213

RESULT 4

US-11-170-653-17

; Sequence 17, Application US/11170653

; Publication No. US20050271769A1

; GENERAL INFORMATION:

; APPLICANT: Danisco A/S

; APPLICANT: Sibbesen, Ole

; APPLICANT: Sorensen, Jens

; TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor

; FILE REFERENCE: 674509-2046

; CURRENT APPLICATION NUMBER: US/11/170,653

; CURRENT FILING DATE: 2005-06-23

; PRIOR FILING DATE: US/10/237,386

; PRIOR FILING DATE: 2002-09-09

; PRIOR APPLICATION NUMBER: PCT/IB01/00426

; PRIOR FILING DATE: 2001-03-08

; PRIOR APPLICATION NUMBER: GB 0005585.5

; PRIOR FILING DATE: 2000-03-08

; PRIOR APPLICATION NUMBER: GB 0015751.1

; PRIOR FILING DATE: 2000-06-27

; NUMBER OF SEQ ID NOS: 66

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 17

; LENGTH: 213

; TYPE: PRT

; ORGANISM: Bacillus circulans

US-11-170-653-17

Query Match 99.7%; Score 1168; DB 7; Length 213;

Best Local Similarity 99.5%; Pred. No. 1.4e-95;

Matches 212; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFKFKQKFLVGLSAAALMSISLFSATASASTDYQWNTDGGIYNAVNGSGGNSVNWNS 60

Db 1 MFKFKQKFLVGLSAAALMSISLFSATASASTDYQWNTDGGIYNAVNGSGGNSVNWNS 60

Qy 61 TGNFVVGKGTGSPFRTINYNAGVWAPNGNGYLTLYGWTRSPLIEYYVVDWSWGTYRPTG 120

Db 61 TGNFVVGKGTGSPFRTINYNAGVWAPNGNGYLTLYGWTRSPLIEYYVVDWSWGTYRPTG 120

Qy 121 TYKGTAKSDGGTYDIYTTTTRYNAPSIDGDRTTFTQYMSVRSQSKRPTGNSNATITFSNHVNA 180

Db 121 TYKGTAKSDGGTYDIYTTTTRYNAPSIDGDRTTFTQYMSVRSQSKRPTGNSNATITFSNHVNA 180

Qy 181 WKSHGMNLGSNWAYQVWATEGYQSSGSSNVTW 213

Db 181 WKSHGMNLGSNWAYQVWATEGYQSSGSSNVTW 213

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Qy 61 TGNFVVGKWTGSPFRRTINYNAGWAPNGNGYLTLYGWTSPLIEYYVVDVSWGTYRPTG 120
Db 61 TGNFVVGKWTGSPFRRTINYNAGWAPNGNGYLTLYGWTSPLIEYYVVDVSWGTYRPTG 120
Qy 121 TYKGTVKSDDGTYDIYTTTRYNAPSIDGDRTTFTQYWSVRSQKPTGNSNATITFSNHVNA 180
Db 121 TYKGTVKSDDGTYDIYTTTRYNAPSIDGDRTTFTQYWSVRSQKPTGNSNATITFSNHVNA 180
Qy 181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTW 213
Db 181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTW 213
```

RESULT 5

```
US-10-517-939-230
; Sequence 230, Application US/10517939
; Publication No. US20060003433A1
; GENERAL INFORMATION:
; APPLICANT: Steer, Brian
; APPLICANT: Callen, Walter
; APPLICANT: Healey, Shaun
; APPLICANT: Hazlewood, Geoff
; APPLICANT: Wu, Di
; APPLICANT: Blum, David
; APPLICANT: Esteghlalian, Alireza
; TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING THEM
; FILE REFERENCE: 564462007901
; CURRENT APPLICATION NUMBER: US/10/517,939
; PRIOR FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: PCT/US03/19153
; PRIOR FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: 60/389,299
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 380
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 230
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Obtained from an environmental sample
```

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Qy 61 TGNFVVGKWTGSPFRRTINYNAGWAPNGNGYLTLYGWTSPLIEYYVVDVSWGTYRPTG 120
Db 61 TGNFVVGKWTGSPFRRTINYNAGWAPNGNGYLTLYGWTSPLIEYYVVDVSWGTYRPTG 120
Qy 61 TGNFVVGKWTGSPFRRTINYNAGWAPNGNGYLTLYGWTSPLIEYYVVDVSWGTYRPTG 120
Db 61 TGNFVVGKWTGSPFRRTINYNAGWAPNGNGYLTLYGWTSPLIEYYVVDVSWGTYRPTG 120
Qy 121 TYKGTVKSDDGTYDIYTTTRYNAPSIDGDRTTFTQYWSVRSQKPTGNSNATITFSNHVNA 180
Db 121 TYKGTVKSDDGTYDIYTTTRYNAPSIDGDRTTFTQYWSVRSQKPTGNSNATITFSNHVNA 180
Qy 181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTW 213
Db 181 WKRYGMNLGSNWYQVLATEGYQSSGSSNVTW 213
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RESULT 6

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US-10-517-939-302
; Sequence 302, Application US/10517939
; Publication No. US20060003433A1
```

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Query Match 94.3%; Score 1104; DB 6; Length 213;
Best Local Similarity 93.0%; Pred. No. 5.5e-90;
Matches 198; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

Qy 1 MFKEKKNFLVGLSAAKMSISLFSATASASTDYQWNTDGGIYNVANGSGNYSVNWNS 60
Db 1 MFKEKKNFLVGLTAAKMSLSLFSANASANTDYQWNTDGGIYNVANGSGNYSVNWNS 60
Qy 61 TGNFVVGKWTGSPFRRTINYNAGWAPNGNGYLTLYGWTSPLIEYYVVDVSWGTYRPTG 120
Db 61 TGNFVVGKWTGSPFRRTINYNAGWAPNGNGYLTLYGWTSPLIEYYVVDVSWGTYRPTG 120
Qy 121 TYKGTVKSDDGTYDIYTTTRYNAPSIDGDRTTFTQYWSVRSQKPTGNSNATITFSNHVNA 180
Db 121 TYKGTVKSDDGTYDIYTTTRYNAPSIDGDRTTFTQYWSVRSQKPTGNSNATITFSNHVNA 180
Qy 181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTW 213
Db 181 WKRYGMNLGSNWYQVLATEGYQSSGSSNVTW 213
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RESULT 7

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US-11-170-653-1
; Sequence 1, Application US/11170653
; Publication No. US20050271769A1
; GENERAL INFORMATION:
; APPLICANT: Danisco A/S
; APPLICANT: Sibbesen, Ole
; APPLICANT: Sorensen, Jens
; TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
; FILE REFERENCE: 674509-2046
; CURRENT APPLICATION NUMBER: US/11/170,653
; CURRENT FILING DATE: 2005-06-23
; PRIOR APPLICATION NUMBER: US/10/237,386
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: PCT/IB01/00426
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: GB 0005585.5
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: GB 0015751.1
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Patent in version 3.0
```

```
; GENERAL INFORMATION:
; APPLICANT: Steer, Brian
; APPLICANT: Callen, Walter
; APPLICANT: Healey, Shaun
; APPLICANT: Hazlewood, Geoff
; APPLICANT: Wu, Di
; APPLICANT: Blum, David
; APPLICANT: Esteghlalian, Alireza
; TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING THEM
; FILE REFERENCE: 564462007901
; CURRENT APPLICATION NUMBER: US/10/517,939
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: PCT/US03/19153
; PRIOR FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: 60/389,299
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 380
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 302
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Obtained from an environmental sample.
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(28)
US-10-517-939-302
```

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Query Match 93.7%; Score 1097; DB 6; Length 213;
Best Local Similarity 92.0%; Pred. No. 2.3e-89;
Matches 196; Conservative 10; Mismatches 7; Indels 0; Gaps 0;

Qy 1 MFKEKKNFLVGLSAAKMSISLFSATASASTDYQWNTDGGIYNVANGSGNYSVNWNS 60
Db 1 MFKEKKNFLVGLTAAKMSLSLFSANASANTDYQWNTDGGIYNVANGSGNYSVNWNS 60
Qy 61 TGNFVVGKWTGSPFRRTINYNAGWAPNGNGYLTLYGWTSPLIEYYVVDVSWGTYRPTG 120
Db 61 TGNFVVGKWTGSPFRRTINYNAGWAPNGNGYLTLYGWTSPLIEYYVVDVSWGTYRPTG 120
Qy 121 TYKGTVKSDDGTYDIYTTTRYNAPSIDGDRTTFTQYWSVRSQKPTGNSNATITFSNHVNA 180
Db 121 TYKGTVKSDDGTYDIYTTTRYNAPSIDGDRTTFTQYWSVRSQKPTGNSNATITFSNHVNA 180
Qy 181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTW 213
Db 181 WKRYGMNLGSNWYQVLATEGYQSSGSSNVTW 213
```

```
; SEQ ID NO 1
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Bacillus subtilis
US-11-170-653-1

Query Match      88.9%; Score 1041; DB 7; Length 185;
Best Local Similarity 100.0%; Pred. No. 1.5e-84;
Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 29 ASTDYQWNTDGGGIVNAVNGSGGNYSVNWSNTGNFVVGKWTGSPRTINYNAGWAP 88
Db 1 ASTDYQWNTDGGGIVNAVNGSGGNYSVNWSNTGNFVVGKWTGSPRTINYNAGWAP 60

Qy 89 NNGYLILYGWTRSPLEIYYVVDWSWGTGTRPGTGTGKTVKSDGGTYDIYTTIRYNAPSIDG 148
Db 61 NNGYLILYGWTRSPLEIYYVVDWSWGTGTRPGTGTGKTVKSDGGTYDIYTTIRYNAPSIDG 120

Qy 149 DRTTFTQVWSVRQSKRPTGSGNATITFSNHNWAKSHGNNLGSNNWAYQVMATEGYQSSGSS 208
Db 121 DRTTFTQVWSVRQSKRPTGSGNATITFSNHNWAKSHGNNLGSNNWAYQVMATEGYQSSGSS 180

Qy 209 NVTVW 213
Db 181 NVTVW 185

RESULT 8
US-10-517-939-198
; Sequence 198, Application US/10517939
; Publication No. US20060003433A1
; GENERAL INFORMATION:
; APPLICANT: Steer, Brian
; APPLICANT: Callen, Walter
; APPLICANT: Healey, Shaun
; APPLICANT: Hazlewood, Geoff
; APPLICANT: Wu, Di
; APPLICANT: Blum, David
; APPLICANT: Esteghlalian, Alireza
; TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING THEM
; TITLE OF INVENTION: AND METHODS FOR MAKING AND USING THEM
; FILE REFERENCE: 564462007901
; CURRENT APPLICATION NUMBER: US/10/517,939
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: PCT/US03/19153
; PRIOR FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: 60/389,299
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 380
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 198
; LENGTH: 211
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Obtained from an environmental sample
; NAME/KEY: SIGNAL
; LOCATION: (1)...(28)
US-10-517-939-198

Query Match      81.4%; Score 953; DB 6; Length 211;
Best Local Similarity 81.7%; Pred. No. 9e-77;
Matches 174; Conservative 13; Mismatches 24; Indels 2; Gaps 2;

Qy 1 MFKFKNFLVGLSAAALMSISLFSATASASTDYQWNTDGGGIVNAVNGSGGNYSVNWSN 60
Db 1 MFKFKKMTVILATWSFGLF-ATTSSATDYQWNTDGGGIVNAVNGSGGNSVTVQN 59

Qy 61 TGNFVVGKWTGSPRTINYNAGWAPNGNGYLTLYGWTRSPLEIYYVVDWSWGTGTRPTG 120
Db 60 TGNFVVGKWTGSPRTINYNAGWAPNGNGYLTLYGWTRNALIEIYYVVDWSWGTGTRPTG 119

; SEQ ID NO 199
; LENGTH: 211
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Obtained from an environmental sample
; NAME/KEY: SIGNAL
; LOCATION: (1)...(28)
US-10-517-939-198

Query Match      81.4%; Score 953; DB 6; Length 211;
Best Local Similarity 81.7%; Pred. No. 9e-77;
Matches 174; Conservative 13; Mismatches 24; Indels 2; Gaps 2;

Qy 1 MFKFKNFLVGLSAAALMSISLFSATASASTDYQWNTDGGGIVNAVNGSGGNYSVNWSN 60
Db 1 MFKFKKMTVILATWSFGLF-ATTSSATDYQWNTDGGGIVNAVNGSGGNSVTVQN 59

Qy 61 TGNFVVGKWTGSPRTINYNAGWAPNGNGYLTLYGWTRSPLEIYYVVDWSWGTGTRPTG 120
Db 60 TGNFVVGKWTGSPRTINYNAGWAPNGNGYLTLYGWTRNALIEIYYVVDWSWGTGTRPTG 119
```

```
Qy 121 TYKGTVKS DGGTYDIYTTIRYNAPSIDGRTTFTQVWSVRQSKRPTGSGNATITFSNHVNA 180
Db 120 TYKGTVTS DGGTYDIYTTIRYNAPSIDGTQ-TFAQYWSVRQSKRATGVNSSITFSNHVNA 178

Qy 181 WKSHGMNLGSNNWAYQVMATEGYQSSGSSNVTVW 213
Db 179 WASKGMNLGSWSYQVLATEGYQSSGSSNVTVW 211

RESULT 9
US-10-517-939-158
; Sequence 158, Application US/10517939
; Publication No. US20060003433A1
; GENERAL INFORMATION:
; APPLICANT: Steer, Brian
; APPLICANT: Callen, Walter
; APPLICANT: Healey, Shaun
; APPLICANT: Hazlewood, Geoff
; APPLICANT: Wu, Di
; APPLICANT: Blum, David
; APPLICANT: Esteghlalian, Alireza
; TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING THEM
; TITLE OF INVENTION: AND METHODS FOR MAKING AND USING THEM
; FILE REFERENCE: 564462007901
; CURRENT APPLICATION NUMBER: US/10/517,939
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: PCT/US03/19153
; PRIOR FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: 60/389,299
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 380
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 158
; LENGTH: 214
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Obtained from an environmental sample
; NAME/KEY: SIGNAL
; LOCATION: (1)...(29)
US-10-517-939-158

Query Match      79.7%; Score 933.5; DB 6; Length 214;
Best Local Similarity 80.4%; Pred. No. 4.6e-75;
Matches 172; Conservative 12; Mismatches 29; Indels 1; Gaps 1;

Qy 1 MFKFKNFLVGLSAAALMS-ISLFSATASASTDYQWNTDGGGIVNAVNGSGGNYSVNWS 59
Db 1 MFKLSKKILAVLLTISMSFISLFAVTAYASTDYQWNTDGGGTVNATNGSDGNSVWS 60

Qy 60 NTGNFVVGKWTGSPRTINYNAGWAPNGNGYLTLYGWTRSPLEIYYVVDWSWGTGTRPT 119
Db 61 NCGNFVVGKWTGTSATRVINYNAGAFSPSGNGYALYGTWTRNSLIEIYYVVDWSWGTGTRPT 120

Qy 120 GTYKGTVKSDGGTYDIYTTIRYNAPSIDGRTTFTQVWSVRQSKRPTGSGNATITFSNHVN 179
Db 121 GTYKGTVTS DGGTYDIYTTIRTNAPSIDGNNTNFTQFWSVRQSKRPIGTNNITITSNHVN 180

Qy 180 AWKSHGMNLGSNNWAYQVMATEGYQSSGSSNVTVW 213
Db 181 AWKSKGNLGSNNWAYQVLATEGYQSSGSSNVTVW 214

RESULT 10
US-11-170-653-19
; Sequence 19, Application US/11170653
; Publication No. US20050271769A1
; GENERAL INFORMATION:
; APPLICANT: Danisco A/S
; APPLICANT: Sibbesen, Ole
; APPLICANT: Sorensen, Jens
; TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
```



```
; FILE REFERENCE: 674509-2046
; CURRENT APPLICATION NUMBER: US/11/170,653
; CURRENT FILING DATE: 2005-06-23
; PRIOR APPLICATION NUMBER: US/10/237,386
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: PCT/IB01/00426
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: GB 0005585.5
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: GB 0015751.1
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 19
; LENGTH: 211
; TYPE: PRT
; ORGANISM: A. caviae
US-11-170-653-19

Query Match      79.3%; Score 929; DB 7; Length 211;
Best Local Similarity 79.3%; Pred. No. 1.1e-74;
Matches 169; Conservative 18; Mismatches 24; Indels 2; Gaps 2;

Qy 1 MFKEKFLVGLSAAALMSISLFSATASAASTDYQNWNTDGGGIVNAVNGSGGNYSVNWSN 60
Db 1 MFKEGKMLMTVLAAASMSFGVFAATSSAA-TDYQNWNTDGGGTVNAVNGSGGNYSVSQN 59

Qy 61 TGNFVVGKWTGSPFRITNAGVWAPNGNGYLTLYGWTRSPLEIYYVVDVSWGTYRPTG 120
Db 60 TGNFVVGKWTGYTPNRVNVNAGVAFPSGNGYLTLYGWTRNALIYYVVDVSWGTYRPTG 119

Qy 121 TYGTVKSDGGTYDIYTTTTRYNAPSIDGDRITFTQYWSVRQSKRPTGSGNATITFSNHVNA 180
Db 120 TYGTVNSDGGTYDIYTTTMRYNAPSIDGTQ-TFPQYWSVRQSKRPTGVSNTITFSNHVNA 178

Qy 181 WSKGMNLGSNWAYQVMATEGYQSSGSSNVTVW 213
Db 179 WPSKGMVNLGNSYQVMATEGYQSSGSNANVTW 211
```

```
RESULT 11
US-10-517-939-208
; Sequence 208, Application US/10517939
; Publication No. US20060003433A1
; GENERAL INFORMATION:
; APPLICANT: Steer, Brian
; APPLICANT: Callen, Walter
; APPLICANT: Healey, Shaun
; APPLICANT: Hazlewood, Geoff
; APPLICANT: Wu, Di
; APPLICANT: Blum, David
; APPLICANT: Esteghalian, Alireza
; TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING THEM
; TITLE OF INVENTION: AND METHODS FOR MAKING AND USING THEM
; FILE REFERENCE: 564462007901
; CURRENT APPLICATION NUMBER: US/10/517,939
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: PCT/US03/19153
; PRIOR FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: 60/389,299
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 380
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 208
; LENGTH: 210
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Obtained from an environmental sample
; NAME/KEY: SIGNAL
; LOCATION: (1)...(27)
US-10-517-939-208
```

```
Query Match      79.2%; Score 927; DB 6; Length 210;
Best Local Similarity 80.1%; Pred. No. 1.7e-74;
Matches 169; Conservative 14; Mismatches 26; Indels 2; Gaps 2;

Qy 3 KFKKNFLVGLSAAALMSISLFSATASAASTDYQNWNTDGGGIVNAVNGSGGNYSVNWSNTG 62
Db 2 KLKKMLTLLLTASMSFGLFGATSSAA-TDYQWNTDGGGTVNAVNGSGGNYSVTWQNSG 60

Qy 63 NFVVGKWTGSPERTINYNAGVWAPNGNGYLTLYGWTRSPLEIYYVVDVSWGTYRPTGY 122
Db 61 NFVVGKWSVGSNRTINYNAGIWEPSGNGYLTLYGWTRNSLIEYYVVDVSWGTYRPTGTH 120

Qy 123 KGTVKSDDGGTYDIYTTTTRYNAPSIDGDRITFTQYWSVRQSKRPTGSGNATITFSNHVNAWK 182
Db 121 KGTVNSDGGTYDIYTTTMRYNAPSIDGTQ-TFQYWSVRQSKRPTGSGNVSIITFSNHVNAWR 179

Qy 183 SHGMNLGSNWAYQVMATEGYQSSGSSNVTVW 213
Db 180 SKGMNLGSSYQVLATEGYQSSGRSNVTW 210

RESULT 12
US-11-170-653-18
; Sequence 18, Application US/11170653
; Publication No. US20050271769A1
; GENERAL INFORMATION:
; APPLICANT: Danisco A/S
; APPLICANT: Sorensen, Ole
; APPLICANT: Sorensen, Jens
; TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
; FILE REFERENCE: 674509-2046
; CURRENT APPLICATION NUMBER: US/11/170,653
; CURRENT FILING DATE: 2005-06-23
; PRIOR APPLICATION NUMBER: US/10/237,386
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: PCT/IB01/00426
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: GB 0005585.5
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: GB 0015751.1
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 18
; LENGTH: 211
; TYPE: PRT
; ORGANISM: Bacillus stearothermophilus
US-11-170-653-18
```

```
Query Match      77.5%; Score 907.5; DB 7; Length 211;
Best Local Similarity 79.2%; Pred. No. 8.6e-73;
Matches 168; Conservative 12; Mismatches 29; Indels 3; Gaps 3;

Qy 3 KFKKNFLVGLSAAALMSISLFSATASAASTDYQNWNTDGGGIVNAVNGSGGNYSVNWSNTG 62
Db 2 KLKKMLTLLLTASMSFGLFGATSSAA-TDYQWNTDGGGTVNAVNGSGGNYSVTWQNTG 60

Qy 63 NFVVGKWTGSPERTINYNAGVWAPNGNGYLTLYGWTRSPLEIYYVVDVSWGTYRPTGY 122
Db 61 NFVVGKWTGSPNRVINYNAGIWEPSGNGYLTLYGWTRNALIYYVVDVSWGTYRATGNY 120

Qy 123 K-GTVKSDGGTYDIYTTTTRYNAPSIDGDRITFTQYWSVRQSKRPTGSGNATITFSNHVNAW 181
Db 121 ESGTVNSDGGTYDIYTTTMRYNAPSIDGTQ-TFQYWSVRQSKRPTGSGNVSIITFSNHVNAW 179

Qy 182 KSHGMNLGSNWAYQVMATEGYQSSGSSNVTVW 213
Db 180 RSKGMNLGSSWAYQVLATEGYQSSGRSNVTW 211
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```
RESULT 13
US-10-517-939-190
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```
; Sequence 190, Application US/10517939
; Publication No. US20060003433A1
; GENERAL INFORMATION:
; APPLICANT: Steer, Brian
; APPLICANT: Callen, Walter
; APPLICANT: Healey, Shaun
; APPLICANT: Hazlewood, Geoff
; APPLICANT: Wu, Di
; APPLICANT: Blum, David
; APPLICANT: Esteghalalian, Alireza
; TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING THEM
; FILE REFERENCE: 564462007901
; CURRENT APPLICATION NUMBER: US/10/517,939
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: PCT/US03/19153
; PRIOR FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: 60/389,299
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 380
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 190
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Obtained from an environmental sample
US-10-517-939-190

Query Match 75.7%; Score 886; DB 6; Length 189;
Best Local Similarity 84.0%; Pred. No. 5.8e-71; Indels 0; Gaps 0;
Matches 158; Conservative 11; Mismatches 19;

Qy 26 ASAASTDYQWNTDGGGIVNAVNGSGGNYSYNWNTGNFVVGKGTGSPPTINYNAGV 85
Db 2 ALMASTDYQWNTDGGGIVNAVNGSGGNYSYSWNSCGNFVVGKGTGTSATRVYNAGA 61

Qy 86 WAPNGNYLYGWTRSPRLIEYYVVDWSGTYRPTGTGTYKSDGGTYDIYTTTRYNAPS 145
Db 62 FSPSGNGYLYGWTRNSLIEYYVVDWSGTYRPTGTGTYKSDGGTYDIYTTTRYNAPS 121

Qy 146 IDGRTTFTQWSVRQSKRPTGSGNATITFSNHNVAWSKGNLGSNNWAYQVMATEGYQSS 205
Db 122 IDGNNTTFTQWSVRQSKRPTGNTTITFSNHNVAWSKGNLGSNNWAYQVMATEGYQSS 181

Qy 206 GSSNVTVW 213
Db 182 GYSNVTVW 199

RESULT 14
US-10-517-939-252
; Sequence 252, Application US/10517939
; Publication No. US20060003433A1
; GENERAL INFORMATION:
; APPLICANT: Steer, Brian
; APPLICANT: Callen, Walter
; APPLICANT: Healey, Shaun
; APPLICANT: Hazlewood, Geoff
; APPLICANT: Wu, Di
; APPLICANT: Blum, David
; APPLICANT: Esteghalalian, Alireza
; TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING THEM
; FILE REFERENCE: 564462007901
; CURRENT APPLICATION NUMBER: US/10/517,939
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: PCT/US03/19153
; PRIOR FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: 60/389,299
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 380
; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 252
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Obtained from an environmental sample
US-10-517-939-252

Query Match 74.6%; Score 873.5; DB 6; Length 184;
Best Local Similarity 83.2%; Pred. No. 7e-70; Indels 1; Gaps 1;
Matches 153; Conservative 15; Mismatches 15;

Qy 30 STDYQWNTDGGGIVNAVNGSGGNYSYNWNTGNFVVGKGTGSPPTINYNAGVWAPN 89
Db 2 ATDYQWNTDGGGIVNAVNGSGGNYSVTWNSGDFVVGKGSVSPRTINYNAGIWEPS 61

Qy 90 GNGYLYLYGWTRSPRLIEYYVVDWSGTYRPTGTGTYKSDGGTYDIYTTTRYNAPSIDGD 149
Db 62 GNGYLYLYGWTRNSLIEYYVVDWSGTYRPTGTGTYKSDGGTYDIYTTTRYNAPSIDGT 121

Qy 150 RTTFTQWSVRQSKRPTGSGNATITFSNHNVAWSKGNLGSNNWAYQVMATEGYQSSSSN 209
Db 122 Q-TFQWFWSVRQSKRPTGSGNVSITFSNHNVAWSKGNLGSNWSYQVLATEGYQSSGRSN 180

Qy 210 VTVW 213
Db 181 VTVW 184

RESULT 15
US-10-517-939-380
; Sequence 380, Application US/10517939
; Publication No. US20060003433A1
; GENERAL INFORMATION:
; APPLICANT: Steer, Brian
; APPLICANT: Callen, Walter
; APPLICANT: Healey, Shaun
; APPLICANT: Hazlewood, Geoff
; APPLICANT: Wu, Di
; APPLICANT: Blum, David
; APPLICANT: Esteghalalian, Alireza
; TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING THEM
; FILE REFERENCE: 564462007901
; CURRENT APPLICATION NUMBER: US/10/517,939
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: PCT/US03/19153
; PRIOR FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: 60/389,299
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 380
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 380
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated polypeptide.
US-10-517-939-380

Query Match 72.1%; Score 844; DB 6; Length 189;
Best Local Similarity 81.4%; Pred. No. 2.8e-67; Indels 0; Gaps 0;
Matches 153; Conservative 10; Mismatches 25;

Qy 26 ASAASTDYQWNTDGGGIVNAVNGSGGNYSYNWNTGNFVVGKGTGSPPTINYNAGV 85
Db 2 ALMASTDYQWNTDGGGIVNAVNGSGGNYSYSWNSCGNFVVGKGTGTSATRVYNAGA 61

Qy 86 WAPNGNYLYGWTRSPRLIEYYVVDWSGTYRPTGTGTYKSDGGTYDIYTTTRYNAPS 145
Db 62 FSPVGNAYLYGWTRNSLIEYYVVDWSGTYRPTGTGTYKSDGGTYDIYTTTRYNAPS 121

Qy 146 IDGRTTFTQWSVRQSKRPTGSGNATITFSNHNVAWSKGNLGSNNWAYQVMATEGYQSS 205
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Db 122 IDGNITTFQFWSVRQSRPIGTNNITTFSSHVNAAKSGMNLGSSWSYQVLATEGYOSS 181
Qy 206 GSSNVTW 213
Db 182 GYSNVTW 189

Search completed: February 3, 2006, 09:13:20
Job time : 8 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 3, 2006, 09:12:23 ; Search time 79 Seconds
(without alignments)
1126.552 Million cell updates/sec

Title: US-10-626-724-5

Perfect score: 1171
Sequence: 1 MFKFKNFLVGLSALMSIS.....YQVMATEGYQSSGSNTVTW 213

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.Main:*
1: /cgm2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgm2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
3: /cgm2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
4: /cgm2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
5: /cgm2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
6: /cgm2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1171	100.0	213	4	US-10-237-386-16
2	1171	100.0	213	5	US-10-626-583-5
3	1171	100.0	213	5	US-10-626-724-5
4	1168	99.7	213	4	US-10-237-386-17
5	1161	99.1	213	5	US-10-626-583-11
6	1161	99.1	213	5	US-10-626-724-11
7	1154	98.5	213	5	US-10-626-583-7
8	1154	98.5	213	5	US-10-626-724-7
9	1149	98.1	213	5	US-10-626-583-9
10	1149	98.1	213	5	US-10-626-724-9
11	1130	96.5	213	5	US-10-626-583-3
12	1130	96.5	213	5	US-10-626-724-3
13	1041	88.9	185	4	US-10-307-441-5
14	1041	88.9	185	4	US-10-237-386-1
15	1041	88.9	185	6	US-11-088-725A-32
16	1041	88.9	197	4	US-10-442-148A-10
17	1041	88.9	360	4	US-10-442-148A-11
18	1038	88.6	185	4	US-10-307-441-3
19	1038	88.6	185	4	US-11-088-725A-30
20	929	79.3	211	4	US-10-237-386-19
21	907.5	77.5	211	4	US-10-237-386-18
22	885	75.6	185	6	US-11-018-645-2
23	885	75.6	186	6	US-11-018-645-14
24	826.5	70.6	192	6	US-11-018-645-8
25	825	70.5	186	6	US-11-018-645-16
26	686.5	58.6	197	6	US-11-018-645-4
27	686.5	58.6	198	6	US-11-018-645-18

28	663.5	56.7	241	4	US-10-237-386-43	Sequence 43, Appl
29	659	56.3	240	4	US-10-237-386-42	Sequence 42, Appl
30	646	55.2	242	4	US-10-237-386-41	Sequence 41, Appl
31	645.5	55.1	239	4	US-10-237-386-40	Sequence 40, Appl
32	640.5	54.7	189	4	US-10-307-441-13	Sequence 13, Appl
33	640.5	54.7	189	6	US-11-088-725A-40	Sequence 40, Appl
34	636	54.3	344	3	US-09-770-621-2	Sequence 2, Appl
35	636	54.3	344	4	US-10-286-993-2	Sequence 2, Appl
36	627.5	53.6	191	6	US-11-088-725A-44	Sequence 44, Appl
37	622	53.1	228	4	US-10-237-386-39	Sequence 39, Appl
38	621	53.0	240	4	US-10-237-386-38	Sequence 38, Appl
39	618.5	52.8	191	4	US-10-307-441-11	Sequence 11, Appl
40	618.5	52.8	191	6	US-11-088-725A-39	Sequence 39, Appl
41	617.5	52.7	234	4	US-10-213-990-69	Sequence 69, Appl
42	587	50.1	191	4	US-10-307-441-10	Sequence 10, Appl
43	587	50.1	191	6	US-11-088-725A-38	Sequence 38, Appl
44	581	49.6	225	4	US-10-237-386-36	Sequence 36, Appl
45	573.5	49.0	189	4	US-10-307-441-19	Sequence 19, Appl

ALIGNMENTS

RESULT 1
US-10-237-386-16
; Sequence 16, Application US/10237386
; Publication No. US20030180895A1
; GENERAL INFORMATION:
; APPLICANT: Danisco A/S
; APPLICANT: Sibbesen, Ole
; APPLICANT: Sorensen, Jens
; TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
; FILE REFERENCE: 674509-2046
; CURRENT APPLICATION NUMBER: US/10/237,386
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: PCT/IB01/00426
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: GB 0005585.5
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: GB 0015751.1
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 16
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Bacillus subtilis
US-10-237-386-16

Query Match	100.0%	Score 1171;	DB 4;	Length 213;
Best Local Similarity	100.0%	Pred. No. 1.5e-96;		
Matches 213;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MFKFKNFLVGLSALMSISLFSATASASTDYQNWTDGGGINAVNNGSGNYSVNWNS	60	
Db	1	MFKFKNFLVGLSALMSISLFSATASASTDYQNWTDGGGINAVNNGSGNYSVNWNS	60	
Qy	61	TGNFVVGKGTGGTGGPFRITINYNAGVWAPNGNYLTLYGWTSPILIEYVVDWSWGTYRPTG	120	
Db	61	TGNFVVGKGTGGTGGPFRITINYNAGVWAPNGNYLTLYGWTSPILIEYVVDWSWGTYRPTG	120	
Qy	121	TYKGTWKSDDGTYYITTYTRYNAPSIDGDRITFTQYMSVRQSKRPTGSNATITFSNHVNA	180	
Db	121	TYKGTWKSDDGTYYITTYTRYNAPSIDGDRITFTQYMSVRQSKRPTGSNATITFSNHVNA	180	
Qy	181	WKGHGMNLGNSWAYQVMATEGYQSSGSNTVTW	213	
Db	181	WKGHGMNLGNSWAYQVMATEGYQSSGSNTVTW	213	

No Dbl. rat.
c
time.

RESULT 2
US-10-626-583-5
; Sequence 5, Application US/10626583

Publication No. US20040234998A1
GENERAL INFORMATION:
APPLICANT: SIBBESEN, OLE
TITLE OF INVENTION: PROTEINS
FILE REFERENCE: 078883/0132
CURRENT APPLICATION NUMBER: US/10/626.583
CURRENT FILING DATE: 2003-07-25
PRIOR APPLICATION NUMBER: US/09/869,155
PRIOR FILING DATE: 2001-10-01
PRIOR APPLICATION NUMBER: PCT/IB99/02071
PRIOR FILING DATE: 1999-12-17
PRIOR APPLICATION NUMBER: GB 9828599.2
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: GB 9907805.7
PRIOR FILING DATE: 1999-04-06
PRIOR APPLICATION NUMBER: GB 9908645.6
PRIOR FILING DATE: 1999-04-15
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 5
LENGTH: 213
TYPE: PRT
ORGANISM: Bacillus subtilis
US-10-626-583-5

Query Match 100.0%; Score 1171; DB 5; Length 213;
Best Local Similarity 100.0%; Pred. No. 1.5e-96;
Matches 213; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFKFKNFLVGLSALMSISLFSATASASTDYQWNTDGGGIYNAVNGSGGYSVNWNS 60
Db 1 MFKFKNFLVGLSALMSISLFSATASASTDYQWNTDGGGIYNAVNGSGGYSVNWNS 60

Qy 61 TGNFVVGKGTGSPFRTINYNAGVWAPNGNGYLLYGWTRSPLEIYYVVDVDSWGTYRPTG 120
Db 61 TGNFVVGKGTGSPFRTINYNAGVWAPNGNGYLLYGWTRSPLEIYYVVDVDSWGTYRPTG 120

Qy 121 TYKGTVKSDGGTYDIYTTTRYNAPSIDGDRFTTFQYWSVRQSKRPTGNSNATITFSNHVA 180
Db 121 TYKGTVKSDGGTYDIYTTTRYNAPSIDGDRFTTFQYWSVRQSKRPTGNSNATITFSNHVA 180

Qy 181 WKSHGMNLGSNWAYQVWATEGYQSSGSSNVTW 213
Db 181 WKSHGMNLGSNWAYQVWATEGYQSSGSSNVTW 213

RESULT 3
US-10-626-724-5
Sequence 5, Application US/10626724
Publication No. US20050079573A1
GENERAL INFORMATION:
APPLICANT: SIBBESEN, OLE
TITLE OF INVENTION: PROTEINS
FILE REFERENCE: 078883/0132
CURRENT APPLICATION NUMBER: US/10/626.724
CURRENT FILING DATE: 2003-07-25
PRIOR APPLICATION NUMBER: US/09/869,155
PRIOR FILING DATE: 2001-06-25
PRIOR APPLICATION NUMBER: PCT/IB99/02071
PRIOR FILING DATE: 1999-12-17
PRIOR APPLICATION NUMBER: GB 9828599.2
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: GB 9907805.7
PRIOR FILING DATE: 1999-04-06
PRIOR APPLICATION NUMBER: GB 9908645.6
PRIOR FILING DATE: 1999-04-15
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 5
LENGTH: 213
TYPE: PRT

ORGANISM: Bacillus subtilis
US-10-626-724-5

Query Match 100.0%; Score 1171; DB 5; Length 213;
Best Local Similarity 100.0%; Pred. No. 1.5e-96;
Matches 213; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFKFKNFLVGLSALMSISLFSATASASTDYQWNTDGGGIYNAVNGSGGYSVNWNS 60
Db 1 MFKFKNFLVGLSALMSISLFSATASASTDYQWNTDGGGIYNAVNGSGGYSVNWNS 60

Qy 61 TGNFVVGKGTGSPFRTINYNAGVWAPNGNGYLLYGWTRSPLEIYYVVDVDSWGTYRPTG 120
Db 61 TGNFVVGKGTGSPFRTINYNAGVWAPNGNGYLLYGWTRSPLEIYYVVDVDSWGTYRPTG 120

Qy 121 TYKGTVKSDGGTYDIYTTTRYNAPSIDGDRFTTFQYWSVRQSKRPTGNSNATITFSNHVA 180
Db 121 TYKGTVKSDGGTYDIYTTTRYNAPSIDGDRFTTFQYWSVRQSKRPTGNSNATITFSNHVA 180

Qy 181 WKSHGMNLGSNWAYQVWATEGYQSSGSSNVTW 213
Db 181 WKSHGMNLGSNWAYQVWATEGYQSSGSSNVTW 213

RESULT 4
US-10-237-386-17
Sequence 17, Application US/10237386
Publication No. US20030180895A1
GENERAL INFORMATION:
APPLICANT: Danisco A/S
APPLICANT: Sibbeesen, Jens
TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
FILE REFERENCE: 674509-2046
CURRENT APPLICATION NUMBER: US/10/237,386
CURRENT FILING DATE: 2002-12-06
PRIOR APPLICATION NUMBER: PCT/IB01/00426
PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: GB 0005585.5
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: GB 0015751.1
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PatentIn version 3.0
SEQ ID NO 17
LENGTH: 213
TYPE: PRT
ORGANISM: Bacillus circulans
US-10-237-386-17

Query Match 99.7%; Score 1168; DB 4; Length 213;
Best Local Similarity 99.5%; Pred. No. 2.8e-96;
Matches 212; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFKFKNFLVGLSALMSISLFSATASASTDYQWNTDGGGIYNAVNGSGGYSVNWNS 60
Db 1 MFKFKNFLVGLSALMSISLFSATASASTDYQWNTDGGGIYNAVNGSGGYSVNWNS 60

Qy 61 TGNFVVGKGTGSPFRTINYNAGVWAPNGNGYLLYGWTRSPLEIYYVVDVDSWGTYRPTG 120
Db 61 TGNFVVGKGTGSPFRTINYNAGVWAPNGNGYLLYGWTRSPLEIYYVVDVDSWGTYRPTG 120

Qy 121 TYKGTVKSDGGTYDIYTTTRYNAPSIDGDRFTTFQYWSVRQSKRPTGNSNATITFSNHVA 180
Db 121 TYKGTVKSDGGTYDIYTTTRYNAPSIDGDRFTTFQYWSVRQSKRPTGNSNATITFSNHVA 180

Qy 181 WKSHGMNLGSNWAYQVWATEGYQSSGSSNVTW 213
Db 181 WKSHGMNLGSNWAYQVWATEGYQSSGSSNVTW 213

RESULT 5
US-10-626-583-11

```
; Sequence 11, Application US/10626583
; Publication No. US20040234998A1
; GENERAL INFORMATION:
; APPLICANT: SIBBESEN, OLE
; APPLICANT: SORESENSEN, JENS FRISBAEK
; TITLE OF INVENTION: PROTEINS
; FILE REFERENCE: 078883/0132
; CURRENT APPLICATION NUMBER: US/10/626,583
; CURRENT FILING DATE: 2003-07-25
; PRIOR APPLICATION NUMBER: US/09/869,155
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/IB99/02071
; PRIOR FILING DATE: 1999-12-17
; PRIOR APPLICATION NUMBER: GB 9828599.2
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: GB 9907805.7
; PRIOR FILING DATE: 1999-04-06
; PRIOR APPLICATION NUMBER: GB 9908645.6
; PRIOR FILING DATE: 1999-04-15
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Mutant Xylanase
US-10-626-583-11
```

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Query Match 99.1%; Score 1161; DB 5; Length 213;
Best Local Similarity 99.1%; Pred. No. 1.2e-95;
Matches 211; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFKFKKFLVGLSAAALMSISLFSATASAASTDYQWNTDGGGINVAVNGSGGNYSVNWSN 60
DB 1 MFKFKKFLVGLSAAALMSISLFSATASAASTDYQWNTDGGGINVAVNGSGGNYSVNWSN 60

QY 61 TGNFVVGKWTGSPFRITNNAGVWAPNGNGYLTLYGWTRSPLEIYYVVDVDSWGTYPRTG 120
DB 61 TGNFVVGKWTGSPFRITNNAGVWAPNGNGYLTLYGWTRSPLEIYYVVDVDSWGTYPRTG 120

QY 121 TYKGTVKSDGGTYDIYTTTRYNAPSIDGDRITFTQYWSVRSKRPTGSGNATITFSNHVNA 180
DB 121 TYKGTVKSDGGTYDIYTTTRYNAPSIDGDRITFTQYWSVRSKRPTGSGNATITFSNHVNA 180

QY 181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTVM 213
DB 181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTVM 213
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```
RESULT 6
US-10-626-724-11
; Sequence 11, Application US/10626724
; Publication No. US20050079573A1
; GENERAL INFORMATION:
; APPLICANT: SIBBESEN, OLE
; APPLICANT: SORESENSEN, JENS FRISBAEK
; TITLE OF INVENTION: PROTEINS
; FILE REFERENCE: 078883/0132
; CURRENT APPLICATION NUMBER: US/10/626,724
; CURRENT FILING DATE: 2003-07-25
; PRIOR APPLICATION NUMBER: US/09/869,155
; PRIOR FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: PCT/IB99/02071
; PRIOR FILING DATE: 1999-12-17
; PRIOR APPLICATION NUMBER: GB 9828599.2
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: GB 9907805.7
; PRIOR FILING DATE: 1999-04-06
; PRIOR APPLICATION NUMBER: GB 9908645.6
; NUMBER OF SEQ ID NOS: 19
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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Mutant Xylanase
US-10-626-724-11

Query Match 99.1%; Score 1161; DB 5; Length 213;
Best Local Similarity 99.1%; Pred. No. 1.2e-95;
Matches 211; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFKFKKFLVGLSAAALMSISLFSATASAASTDYQWNTDGGGINVAVNGSGGNYSVNWSN 60
DB 1 MFKFKKFLVGLSAAALMSISLFSATASAASTDYQWNTDGGGINVAVNGSGGNYSVNWSN 60

QY 61 TGNFVVGKWTGSPFRITNNAGVWAPNGNGYLTLYGWTRSPLEIYYVVDVDSWGTYPRTG 120
DB 61 TGNFVVGKWTGSPFRITNNAGVWAPNGNGYLTLYGWTRSPLEIYYVVDVDSWGTYPRTG 120

QY 121 TYKGTVKSDGGTYDIYTTTRYNAPSIDGDRITFTQYWSVRSKRPTGSGNATITFSNHVNA 180
DB 121 TYKGTVKSDGGTYDIYTTTRYNAPSIDGDRITFTQYWSVRSKRPTGSGNATITFSNHVNA 180

QY 181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTVM 213
DB 181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTVM 213
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```
RESULT 7
US-10-626-583-7
; Sequence 7, Application US/10626583
; Publication No. US20040234998A1
; GENERAL INFORMATION:
; APPLICANT: SIBBESEN, OLE
; APPLICANT: SORESENSEN, JENS FRISBAEK
; TITLE OF INVENTION: PROTEINS
; FILE REFERENCE: 078883/0132
; CURRENT APPLICATION NUMBER: US/10/626,583
; CURRENT FILING DATE: 2003-07-25
; PRIOR APPLICATION NUMBER: US/09/869,155
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/IB99/02071
; PRIOR FILING DATE: 1999-12-17
; PRIOR APPLICATION NUMBER: GB 9828599.2
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: GB 9907805.7
; PRIOR FILING DATE: 1999-04-06
; PRIOR APPLICATION NUMBER: GB 9908645.6
; PRIOR FILING DATE: 1999-04-15
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Mutant Xylanase
US-10-626-583-7
```

```
Query Match 98.5%; Score 1154; DB 5; Length 213;
Best Local Similarity 98.1%; Pred. No. 4.9e-95;
Matches 209; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFKFKKFLVGLSAAALMSISLFSATASAASTDYQWNTDGGGINVAVNGSGGNYSVNWSN 60
DB 1 MFKFKKFLVGLSAAALMSISLFSATASAASTDYQWNTDGGGINVAVNGSGGNYSVNWSN 60

QY 61 TGNFVVGKWTGSPFRITNNAGVWAPNGNGYLTLYGWTRSPLEIYYVVDVDSWGTYPRTG 120
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Db 61 TGNFVVGKGTGSPERTINYNAGVWAPNGNGYLTLYGWTRSPLEIYYVVDVSWGTYRPTG 120
Qy 121 TYKGTVKS DGGTYDIYITTRYNAPSIDGDRITFTQYWSVRSQSKRPTGSNATITFSNHVA 180
Db 121 TYKGTVKS DGGTYDIYITTRYNAPSIDGDRITFTQYWSVRSQSKRPTGSNATITFSNHVA 180
Qy 181 WKSHGMNLGSNWAYQVWATEGYQSSGSSNVTW 213
Db 181 WKSHGMNLGSNWAYQVWATEGYQSSGSSNVTW 213

RESULT 8

US-10-626-724-7
; Sequence 7, Application US/10626724
; Publication No. US20050079573A1
; GENERAL INFORMATION:
; APPLICANT: SIBBESEN, OLE
; APPLICANT: SORESEN, JENS FRISBAEK
; TITLE OF INVENTION: PROTEINS
; FILE REFERENCE: 078883/0132
; CURRENT APPLICATION NUMBER: US/10/626,724
; CURRENT FILING DATE: 2003-07-25
; PRIOR APPLICATION NUMBER: US/09/869,155
; PRIOR FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: PCT/IB99/02071
; PRIOR FILING DATE: 1999-12-17
; PRIOR APPLICATION NUMBER: GB 9828599.2
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: GB 9907805.7
; PRIOR FILING DATE: 1999-04-06
; PRIOR APPLICATION NUMBER: GB 9908645.6
; PRIOR FILING DATE: 1999-04-15
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Mutant Xylanase
US-10-626-724-7

Query Match 98.5%; Score 1154; DB 5; Length 213;
Best Local Similarity 98.1%; Pred. No. 4.9e-95;
Matches 209; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
Qy 1 MFKFKNFLVGLSALMSISLFSATASASTDYQWNTDGGGIVNAVNGSGGNYSVNWSN 60
Db 1 MFKFKNFLVGLSALMSISLFSATASASTDYQWNTDGGGIVNAVNGSGGNYSVNWSN 60
Qy 61 TGNFVVGKGTGSPERTINYNAGVWAPNGNGYLTLYGWTRSPLEIYYVVDVSWGTYRPTG 120
Db 61 TGNFVVGKGTGSPERTINYNAGVWAPNGNGYLTLYGWTRSPLEIYYVVDVSWGTYRPTG 120
Qy 121 TYKGTVKS DGGTYDIYITTRYNAPSIDGDRITFTQYWSVRSQSKRPTGSNATITFSNHVA 180
Db 121 TYKGTVKS DGGTYDIYITTRYNAPSIDGDRITFTQYWSVRSQSKRPTGSNATITFSNHVA 180
Qy 181 WKSHGMNLGSNWAYQVWATEGYQSSGSSNVTW 213
Db 181 WKSHGMNLGSNWAYQVWATEGYQSSGSSNVTW 213

RESULT 9

US-10-626-583-9
; Sequence 9, Application US/10626583
; Publication No. US20040234998A1
; GENERAL INFORMATION:
; APPLICANT: SIBBESEN, OLE
; APPLICANT: SORESEN, JENS FRISBAEK
; TITLE OF INVENTION: PROTEINS
; FILE REFERENCE: 078883/0132

; CURRENT APPLICATION NUMBER: US/10/626,583
; CURRENT FILING DATE: 2003-07-25
; PRIOR APPLICATION NUMBER: US/09/869,155
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/IB99/02071
; PRIOR FILING DATE: 1999-12-17
; PRIOR APPLICATION NUMBER: GB 9828599.2
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: GB 9907805.7
; PRIOR FILING DATE: 1999-04-06
; PRIOR APPLICATION NUMBER: GB 9908645.6
; PRIOR FILING DATE: 1999-04-15
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Mutant Xylanase
US-10-626-583-9

Query Match 98.1%; Score 1149; DB 5; Length 213;
Best Local Similarity 97.7%; Pred. No. 1.4e-94;
Matches 208; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
Qy 1 MFKFKNFLVGLSALMSISLFSATASASTDYQWNTDGGGIVNAVNGSGGNYSVNWSN 60
Db 1 MFKFKNFLVGLSALMSISLFSATASASTDYQWNTDGGGIVNAVNGSGGNYSVNWSN 60
Qy 61 TGNFVVGKGTGSPERTINYNAGVWAPNGNGYLTLYGWTRSPLEIYYVVDVSWGTYRPTG 120
Db 61 TGNFVVGKGTGSPERTINYNAGVWAPNGNGYLTLYGWTRSPLEIYYVVDVSWGTYRPTG 120
Qy 121 TYKGTVKS DGGTYDIYITTRYNAPSIDGDRITFTQYWSVRSQSKRPTGSNATITFSNHVA 180
Db 121 TYKGTVKS DGGTYDIYITTRYNAPSIDGDRITFTQYWSVRSQSKRPTGSNATITFSNHVA 180
Qy 181 WKSHGMNLGSNWAYQVWATEGYQSSGSSNVTW 213
Db 181 WKSHGMNLGSNWAYQVWATEGYQSSGSSNVTW 213

RESULT 10

US-10-626-724-9
; Sequence 9, Application US/10626724
; Publication No. US20050079573A1
; GENERAL INFORMATION:
; APPLICANT: SIBBESEN, OLE
; APPLICANT: SORESEN, JENS FRISBAEK
; TITLE OF INVENTION: PROTEINS
; FILE REFERENCE: 078883/0132
; CURRENT APPLICATION NUMBER: US/10/626,724
; CURRENT FILING DATE: 2003-07-25
; PRIOR APPLICATION NUMBER: US/09/869,155
; PRIOR FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: PCT/IB99/02071
; PRIOR FILING DATE: 1999-12-17
; PRIOR APPLICATION NUMBER: GB 9828599.2
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: GB 9907805.7
; PRIOR FILING DATE: 1999-04-06
; PRIOR APPLICATION NUMBER: GB 9908645.6
; PRIOR FILING DATE: 1999-04-15
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic


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; SEQ ID NO 5
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Bacillus subtilis
US-10-307-441-5

Query Match      88.9%; Score 1041; DB 4; Length 185;
Best Local Similarity 100.0%; Pred. No. 5.3e-85;
Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 29 ASTDYQNWTDGGGIVNAVNGSGGNYSVNWSNTGNFVVGKGTWTTGSPFRITNNAGVWAP 88
Db 1 ASTDYQNWTDGGGIVNAVNGSGGNYSVNWSNTGNFVVGKGTWTTGSPFRITNNAGVWAP 60

Qy 89 NNGGYLTLYGWTRSPLEIYYVVDWSWGTYPRTGTYKGTGKSDGGTYDIYTTTRYNAPSIDG 148
Db 61 NNGGYLTLYGWTRSPLEIYYVVDWSWGTYPRTGTYKGTGKSDGGTYDIYTTTRYNAPSIDG 120

Qy 149 DRTTFTQYWSVRQSKRPTGSGNATITFSNHNVAWSHGNNLGSNNWAYQVMATEGYQSSGSS 208
Db 121 DRTTFTQYWSVRQSKRPTGSGNATITFSNHNVAWSHGNNLGSNNWAYQVMATEGYQSSGSS 180

Qy 209 NVTVM 213
Db 181 NVTVM 185

RESULT 14
US-10-237-386-1
; Sequence 1, Application US/10237386
; Publication No. US20030180895A1
; GENERAL INFORMATION:
; APPLICANT: Danisco A/S
; APPLICANT: Sorensen, Jens
; TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
; FILE REFERENCE: 674505-2046
; CURRENT APPLICATION NUMBER: US/10/237,386
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: PCT/IB01/00426
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: GB 0005585.5
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: GB 0015751.1
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 1
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Bacillus subtilis
US-10-237-386-1

Query Match      88.9%; Score 1041; DB 4; Length 185;
Best Local Similarity 100.0%; Pred. No. 5.3e-85;
Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 29 ASTDYQNWTDGGGIVNAVNGSGGNYSVNWSNTGNFVVGKGTWTTGSPFRITNNAGVWAP 88
Db 1 ASTDYQNWTDGGGIVNAVNGSGGNYSVNWSNTGNFVVGKGTWTTGSPFRITNNAGVWAP 60

Qy 89 NNGGYLTLYGWTRSPLEIYYVVDWSWGTYPRTGTYKGTGKSDGGTYDIYTTTRYNAPSIDG 148
Db 61 NNGGYLTLYGWTRSPLEIYYVVDWSWGTYPRTGTYKGTGKSDGGTYDIYTTTRYNAPSIDG 120

Qy 149 DRTTFTQYWSVRQSKRPTGSGNATITFSNHNVAWSHGNNLGSNNWAYQVMATEGYQSSGSS 208
Db 121 DRTTFTQYWSVRQSKRPTGSGNATITFSNHNVAWSHGNNLGSNNWAYQVMATEGYQSSGSS 180

Qy 209 NVTVM 213
Db 181 NVTVM 185
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RESULT 15
US-11-088-725A-32
; Sequence 32, Application US/11088725A
; Publication No. US20050214410A1
; GENERAL INFORMATION:
; APPLICANT: Iogen Bio-Products Corporation
; APPLICANT: White, Theresa C
; APPLICANT: Giroux, Genevieve R
; APPLICANT: Wallace, Katie E.A.
; TITLE OF INVENTION: Modified Xylanases Exhibiting Improved Expression
; FILE REFERENCE: Q80712
; CURRENT APPLICATION NUMBER: US/11/088,725A
; CURRENT FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 60/556,061
; PRIOR FILING DATE: 2004-03-25
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 32
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Bacillus subtilis
US-11-088-725A-32
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Query Match      88.9%; Score 1041; DB 6; Length 185;
Best Local Similarity 100.0%; Pred. No. 5.3e-85;
Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 29 ASTDYQNWTDGGGIVNAVNGSGGNYSVNWSNTGNFVVGKGTWTTGSPFRITNNAGVWAP 88
Db 1 ASTDYQNWTDGGGIVNAVNGSGGNYSVNWSNTGNFVVGKGTWTTGSPFRITNNAGVWAP 60

Qy 89 NNGGYLTLYGWTRSPLEIYYVVDWSWGTYPRTGTYKGTGKSDGGTYDIYTTTRYNAPSIDG 148
Db 61 NNGGYLTLYGWTRSPLEIYYVVDWSWGTYPRTGTYKGTGKSDGGTYDIYTTTRYNAPSIDG 120

Qy 149 DRTTFTQYWSVRQSKRPTGSGNATITFSNHNVAWSHGNNLGSNNWAYQVMATEGYQSSGSS 208
Db 121 DRTTFTQYWSVRQSKRPTGSGNATITFSNHNVAWSHGNNLGSNNWAYQVMATEGYQSSGSS 180

Qy 209 NVTVM 213
Db 181 NVTVM 185
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Search completed: February 3, 2006, 09:13:51
Job time : 80 secs